

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 2, 2004, 10:01:29 ; Search time 195 Seconds
(without alignments)
12987.389 Million cell updates/sec

Title: US-10-035-045-20

Perfect score: 3563

Sequence: 1 agcctggcagtgccctcagg.....tggacacccctgtgaccatc 3563

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112.4	3.2	4134	3	US-09-162-021B-1
2	112.4	3.2	4134	4	US-09-687-477-17
3	112.4	3.2	4134	4	US-09-687-476-17
4	112.4	3.2	4134	4	US-09-687-372-17
5	112.4	3.2	4134	4	US-09-975-553-17
6	112.4	3.2	4134	4	US-10-270-795-17
7	112.4	3.2	4134	4	US-10-270-876-17
8	112.4	3.2	4134	4	US-10-268-051-7
9	111	3.1	2925	4	US-09-695-481-3
10	111	3.1	3234	4	US-09-016-434-1432
11	111	3.1	3809	1	US-08-485-588-3
12	111	3.1	3809	1	US-08-484-565-3
13	111	3.1	3809	2	US-08-480-751-3
14	111	3.1	3809	2	US-08-943-986-3
15	111	3.1	3809	3	US-08-353-784-3
16	111	3.1	3809	3	US-08-484-719B-3
17	111	3.1	3809	3	US-08-546-998-2
18	111	3.1	3809	3	US-08-484-159-3
19	111	3.1	4000	2	US-08-687-289A-2
20	111	3.1	4000	4	US-09-435-897-2
21	111	3.1	5006	1	US-08-485-588-2
22	111	3.1	5006	1	US-08-484-565-2
23	111	3.1	5006	2	US-08-480-751-2
24	111	3.1	5006	2	US-08-943-986-2
25	111	3.1	5006	3	US-08-353-784-2
26	111	3.1	5006	3	US-08-484-719B-2
27	111	3.1	5006	3	US-08-546-998-1

28	111	3.1	5006	3	US-08-484-159-2	Sequence 2, Appli
29	109.2	3.1	2993	3	US-09-361-631-3	Sequence 3, Appli
30	109	3.1	2010	3	US-09-361-631-8	Sequence 4, Appli
31	108.8	3.1	2532	3	US-09-361-631-4	Sequence 8, Appli
32	104.8	2.9	5275	1	US-08-485-588-1	Sequence 1, Appli
33	104.8	2.9	5275	1	US-08-484-565-1	Sequence 1, Appli
34	104.8	2.9	5275	2	US-08-480-751-1	Sequence 1, Appli
35	104.8	2.9	5275	2	US-08-943-986-1	Sequence 1, Appli
36	104.8	2.9	5275	3	US-08-353-784-1	Sequence 1, Appli
37	104.8	2.9	5275	3	US-08-484-719B-1	Sequence 1, Appli
38	104.8	2.9	5275	3	US-08-484-159-1	Sequence 1, Appli
39	101.2	2.8	3384	2	US-08-687-289A-1	Sequence 1, Appli
40	101.2	2.8	3384	4	US-09-435-897-1	Sequence 1, Appli
41	98.6	2.8	3177	3	US-09-134-513-1	Sequence 1, Appli
42	90.4	2.5	2148	5	PCT-US93-01642-1	Sequence 1, Appli
43	82.6	2.3	4131	1	US-08-485-588-4	Sequence 4, Appli
44	82.6	2.3	4131	1	US-08-484-565-4	Sequence 4, Appli
45	82.6	2.3	4131	2	US-08-480-751-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-162-021B-1
; Sequence 1, Application US/09162021B
; Patent No. 6337391
; GENERAL INFORMATION:
; APPLICANT: H. William Harris
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic
; TITLE OF INVENTION: Species and Methods of Use Thereof
; FILE REFERENCE: 2856.1001-007
; CURRENT APPLICATION NUMBER: US/09/162,021B
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: PCT/US97/05031
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 08/622,738
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: squalus acanthias
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (439)...(3522)
US-09-162-021B-1

Query Match 3.2%; Score 112.4; DB 3; Length 4134;
Best Local Similarity 46.3%; Pred. No. 2.9e-13;
Matches 408; Conservative 0; Mismatches 471; Indels 3; Gaps 1;

QY	2422	GACGACATCGCTGCACCTTTTGGCCAGATGAGTGTCTCCCGGACGAGACACGC	2481
DB	2194	GATCAAGTGGTGTACAACTGCCGGAATGTTCTGGTCAATGAGAACACACGTCG	2253
QY	2482	TGCTTCGCGCCGAGGTCTCGGTTCTTGGCATGGGCGCGGCTGTCTGCTGCTGCTC	2541
DB	2254	TGCATGCCAAGGAGATCGAGTACTGTCTGGAGGAGCCCTTCGGGATCGCTTGACC	2313
QY	2542	CTGCTGTGAGCTGGCGCTGGGCTTGTGCTGGCTGTTTGGGGCTGTCTGTTCCACAT	2601
DB	2314	ATCTTCGCGTACTGGGCATCTGATCACCTCTTCTGCTGGGGGCTTTCATCACTGC	2373
QY	2602	CGGACAGCCCACTGTTTACGGCTCGGGGGGCCCCCTGGCCTCTTTGGCTGTGTC	2661
DB	2374	AGGAACACTCCCACTCGTGAAGGGCCACCAACCGGGAGTTGTCTACTGCTGCTCTTC	2433
QY	2662	CTGGGCTGTGTTCTGCTCAGCTCTCTTGTTCCTGCGGAGCCCGCCCTGCCGATGC	2721

2434	Db	CTCATCTGCTGCTTCTCCAGCTCGCTCATCTTCATCGGGAGCCAGGAGCTGGACCTGT	2493
2722	Qy	CTGGCCCAAGACCCCTTGTTCACACTCCCGTCTACGGGCTGCTTGAGCACACTCTTCCTG	2781
2494	Db	CGGCTCCGCCAACCGGCCTTTGGCATCAGCTTCGTCCTGTGCATCTCTGCATCTCTGGTG	2553
2782	Qy	CAGCGGCGGAGATCTTCTGTGAGTCAAACTGCCTCTGAGCTGGGACACGGCTGAGT	2841
2554	Tb	AAGACCAACCGGCTGTGTGGTCTTTCGA--GGCCAAGATCCCCACCAAGCTCCACCGC	2610
2842	Qy	GGCTGCTCGGGGGGCCCTGGGCTGGCTGTGGTGTCTGCTGGCCATGCTGCTGGAGTTC	2903
2611	Db	AAGTGGTGGGCTCAACTGCAATGTTCTCTGGTCTTCTCTGCACTCTGGTGCAATC	2670
2902	Qy	GCACCTGTGACCTGGTACCTGTGGCTTCCCGCGGAGGTGGTGAAGGACTGGCACATG	2961
2671	Db	GTCACTGTCATCATCTGGCTCTACACGGCGCCTCCCTCCAGGTACAGGAACCATGAGCTG	2730
2962	Qy	CTGCCACGGAGGCGTGGTGACTGCGGCACACGCTCCTGGGTCAAGTTCGGCCTTAGCG	3021
2731	Db	GAGGACGAGGTCACTTTCATCACCTGCGAGAGGCTCGCTCAATGGCGCTGGGCTTCCTC	2790
3022	Qy	CAGCCACCAATGCCACGCTGGCTTTCTCTGTTCTCTGGGCACATTTCTGTGTCGGAGC	3081
2791	Db	ATCGGCTACACCTGCCTCTCGCGGCACTGCTTCTTCTTCGCTTCAAGTCCCGTAAG	2850
3082	Qy	CAGCGGGTGTCTAACACGCTGCCGTGGCTCACTTTGGCCATGCTGGGCTACTTCATC	3141
2851	Db	CTGCCGGAGAACTTCAACGAGGCTAAGTTTCATCACCTTCAGCATGTTGATCTTCTTCA	2910
3142	Qy	ACCTGGGTCTCTTTGTGGCCCTCCTGGCCAAATGTCAGTGGTCTCTCAGGCGCGCGTG	3201
2911	Db	GTCTGATCTCTTTCATCCCGGCTATGTGAGCACCTACGGCAAGTTTGTGTCGGCGTG	2970
3202	Qy	CAGATGGGCGCCCTCTCTGCTGTGTCTCTGGGCATCTGGCTGCCTTCCACCTGCCGAGG	3261
2971	Db	GAGGTGATGCCATCTTGGCTCCAGTCTGGGCTGTGGGCTGCATTTACTTCAACAAG	3030
3262	Qy	TGTTACTGCTCATAGGGCACGACGGGCTCAACACCCCCGAG	3303
3031	Tb	TGTTACATCATCTGTTCAAGCCGTGCGGTAAACCATCAG	3072

RESULT 2

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US-09-687-477-17
; Sequence 17, Application US/09687477
; Patent No. 6463883
; GENERAL INFORMATION:
; APPLICANT: AquaBio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betra, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; TITLE OF INVENTION: Fish
; FILE REFERENCE: 2213.1004-000
; CURRENT APPLICATION NUMBER: US/09/687,477
; CURRENT FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-09-687-477-17

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	QY	2482	TGCTTCGGCCGACAGTCTCGGTTCCTGGCATCAGCGCGCGCGCTGTGCTGTCTGCTGC	2541
	Db	2254	TGCATCGCCAAAGAGATCAGTACCCTGTCTGTGGA CGAGGCCCTTCGGATCGCTCTGACC	2313
	QY	2542	CTTGCTGCTGAGCTCGCGCTGGCCCTTTGCTGGCTGCTTTTGGGCTGTTTCGTTCAACAT	2601
	Db	2314	ATCTTCGCGTACTGGGCATCTGATCACCTCTTCGTGCTGGGGTCTTTCATCAAGTTC	2373
	QY	2602	CGGGAACAGCCCACCTGTTCAAGGCTCGGGGGGGCCCCCTGGCTGCTTTGGCTGGTGTC	2661
	Db	2374	AGGAACACTCCCATCGTAGAGCCACCAACCGGAGTTGTCTACTA CTTGCTGCTTCTTC	2433
	QY	2662	CTGGGCTGGTCTGCTCCTAGCGTCTCTGTTTCCCTGGCCAGCCAGCCCTCGCCGATGC	2721
	Db	2434	CTCATCTGCTGCTTCTCCAGCTCTGCTCATCTTCATTCGGCGAGCCAGGACTGGACCTGT	2499
	QY	2722	CTGGCCACGACGACCTTTGTCCACCTCCGCTCAAGGGGCTGCTGAGACA CATCTTCCCTG	2781
	Db	2494	CGSCTCCGCCAACCGGCCCTTTGGCATCAGCTTCGTCTCTGTGCATCTCTCTGCATCTCTGGTG	2553
	QY	2782	CAGGCGCCGAGATCTTCTGTGAGTCAGAACTGCCTCTGAGCTGGCAGACCGGTGAGT	2841
	Db	2554	AAGACCAAACGGGTGCTGTGTGTTTCGA ---GGCCAAGATCCCCACCAAGCTTCCACCGC	2610
	QY	2842	GCTGCTCCTCGGGGGCCCTGGGCTGGCTGGTGGTGTCTGCTGCGCCATGCTGTGTGAGGTC	2901
	Db	2611	AA GTGGGTGGGCCCTCAACCTGCAGTTCTCTCTGCTTCTCTCTGTCATCTCTGGTCAAAATC	2670
	QY	2902	GC ACTGTGCACCTGTGTACCTGTGGCTTTCCGCCGAGGTGGTGA CGGACTGGCACATG	2961
	Db	2671	GTCACTGCATCATCTGGCTCTACACGGCGCTCCCTCCAGCTTACAGGAACCATGAGCTG	2730
	QY	2962	CTGCCACGAGAGCGGTGTGTGCATCTCGCGCACACGCTCCTGGGTGAGCTTCGSCCTAGCG	3021
	Db	2731	GAGGACGAGATCATCTTCATCACCCTCGACGAGGGCTCGCTCATGGCGCTGGGCTTCTCTC	2790
	QY	3022	CAGCCACCAATGCCAGCTGGCTTCTCTGCTTCTCTGGGCACTTTTCTGTGTGCGGAGC	3081
	Db	2791	ATCGGTACACCTGCTCTCTCGCGCCATCTGCTTCTTCTTTCGCTTCAAGTCCCGTAAG	2850
	QY	3082	CAGCCGGCTGTCAACACCGTGCCTGGGCTCACCTTTGCCATGTCTGGCTACTTCATC	3141
	Db	2851	CTCGCGAGAACTTCAACGAGGCTAAGTTTCATCACCTTCAGCATGTGTGATCTTCTTCAATC	2910
	QY	3142	ACCTGGGTCTCTTTGTGCGCCCTCCTGGCCAAATGTGACAGTGGTTCCTCA GCGCGCGCTG	3201
	Db	2911	GTCTGSA TCTCTTCATCCCGGCTATGTGAGCACCTTACGGCAAGTTTGTGTGCGGCTG	2970
	QY	3202	CAGATGGGCGCCCTCTCTGCTGTGTCTGGGCATCTCTGGCTGCTCTTCCACCTTCCOAGG	3261
	Db	2971	GAGTGATTGGCATCTTGGCCTCCAGCTTCGGGCTGCTGGGCTGCATTTACTTCAACAAG	3030
	QY	3262	TGTTACCTGTCTATGGGCGACGAGGCTCAACACCCCCGAG	3303
	b	3031	TGTTACATCATCTGTTTCAAGCCCGTGGCGGTGCGGTAAACCATCAG	3072

RESULT 3

; Sequence 17, Application US/09687476
 ; Patent No. 645792
 ; GENERAL INFORMATION:
 ; APPLICANT: AquaBio Product Sciences, LLC
 ; APPLICANT: Harris, H. William, Jr.
 ; APPLICANT: Russell, David R.
 ; APPLICANT: Nearing, Jacqueline
 ; APPLICANT: Betka, Marlies
 ; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
 ; TITLE OF INVENTION: Fish
 ; FILE REFERENCE: 2213.2001-000
 ; CURRENT APPLICATION NUMBER: US/09/687,476
 ; CURRENT FILING DATE: 2000-10-22

GENERAL INFORMATION:

APPLICANT: Harris, H. William
APPLICANT: Jury, Steven
APPLICANT: Russell, David R.
APPLICANT: Nearing, Jacqueline A
APPLICANT: Betka, Marlies
APPLICANT: Linley, Timothy
APPLICANT: Brown, Edward M
TITLE OF INVENTION: Methods for Growing and Imprinting Fish Using an Odorant
FILE REFERENCE: 2213.2004-001
CURRENT APPLICATION NUMBER: US/10/268,051
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 60/328,464
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 4134
TYPE: DNA
ORGANISM: Squalus acanthias
US-10-268-051-7

Query Match 3.2%; Score 112.4; DB 4; Length 4134;

Best Local Similarity 46.3%; Pred. No. 2.9e-13;

Matches 408; Conservative 0; Mismatches 471; Indels 3; Gaps 1;

QY 2422 GACACATCGCTGACACTTTTGGCCAGGATGAGTGGTCCCGGAGCGACACAGC 2481
DB |||||
QY 2194 GATGCAAGTGGGTACAAAGTGCCCGAATGATTTCTGGTGAATGAGAACACACGTG 2253
DB |||||
QY 2482 TGCTTCGCGCAGGTCTCGGTCTCTGCGATGGGCGAGCGGTGTGCTGCTGCTGTC 2541
DB |||||
QY 2254 TGCATGCGCAAGAGATGAGTACTGTGCTGGAGGAGCCCTCGGGATCGCTTGACC 2313
DB |||||
QY 2542 CTGCTGTGAGCCTGGCGCTGGGCTTGTGTGCTGCTTGGGCTGTGCTTACCAAT 2601
DB |||||
QY 2314 ATCTTGGCGTACTGGGATCTGATACCTCTCTGCTGGGCTCTTCATCAAGTTC 2373
DB |||||
QY 2602 CGGACAGCCACTGGTTACAGCTCGGGGGGCGGCTGGGCTGTGGCTGGTGGTGC 2661
DB |||||
QY 2374 AGGAACACTCCCATCGTGAAGGCGCACCAACCGGAGTTGTCTACCTGCTCTTCTCC 2433
DB |||||
QY 2662 CTGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2721
DB |||||
QY 2434 CTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2493
DB |||||
QY 2722 CTGGCCAGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2781
DB |||||
QY 2494 CGGCTCGGCCAACCGGCTTTGGCATCAGCTTGGTCTGCTGCTGCTGCTGCTGCTGCTG 2553
DB |||||
QY 2782 CAGGGCGCGAGATCTTCTGCTGAGTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2841
DB |||||
QY 2554 AAGACCAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2610
DB |||||
QY 2842 GCTGCTGCTGCGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2901
DB |||||
QY 2611 AAGTGGTGGGCTCAACTGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2670
DB |||||
QY 2902 GACTGTGCACTGGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2961
DB |||||
QY 2671 GTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2730
DB |||||
QY 2962 CTGCCACGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3021
DB |||||
QY 2731 GAGACGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2790
DB |||||
QY 3022 CACGCCACCAATGCGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3081
DB |||||
QY 2791 ATCGGCTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2850
DB |||||
QY 3082 CAGCGGGGTGTACACCGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3141
DB |||||
QY 2851 CTGCCGAGAACTTCAACGAGGCTAAGTTTCACTTCACTTCACTTCACTTCACTTCACTT 2910
DB |||||

QY 3142 ACCTGGGTCTCTTTGTGGCCCTCTCTGGCAATGTGCAGTGGTCTCTCAGGCCCGCGTG 3201
DB |||||
QY 2911 GTCTGGATCTCTTTCATCCCGCTATGTGACACCTACGCAAGTTGTGTGGCGGTG 2970
DB |||||
QY 3202 CAGATGGCGCCCTCTCTGCTGTGTCTCTGGGCACTCTGCTGCTTCCACCTGCCGAGG 3261
DB |||||
QY 2971 GAGTGATTGCCATCTCTGGCTCCAGCTTGGGCTGTGGCTGCACTTACTTCAACAAG 3030
DB |||||
QY 3262 TGTACTGTCTCATGGGAGGAGGAGGCTCAACACCCCGAG 3303
DB |||||
QY 3031 TGTATCATCATCTCTGTTCAAGCGCTGCCGTAACACCATCGAG 3072
DB |||||

RESULT 9

US-09-695-481-3

Sequence 3, Application US/09695481

Patent No. 6534287

GENERAL INFORMATION:

APPLICANT: STORMANN, THOMAS M.

APPLICANT: LEVINTHAL, CYNTHIA

APPLICANT: STORJOHANN, LAURA

APPLICANT: HAMMERLAND, LAURIE G.

APPLICANT: KRAPCHO, KAREN J.

APPLICANT: NPS PHARMACEUTICALS, INC.

TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR

FILE REFERENCE: 1094.2.6

CURRENT APPLICATION NUMBER: US/09/695,481

CURRENT FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: 60/161,481

PRIOR FILING DATE: 1999-10-25

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3

LENGTH: 2925

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(2925)

OTHER INFORMATION: Description of Artificial Sequence:Chimeric

OTHER INFORMATION: molecule comprising portions of the human calcium

OTHER INFORMATION: receptor and human mGluR5d.

US-09-695-481-3

Query Match 3.1%; Score 111; DB 4; Length 2925;

Best Local Similarity 51.7%; Pred. No. 5.1e-13;

Matches 286; Conservative 0; Mismatches 255; Indels 12; Gaps 1;

QY 938 CAGTCAAGCTACGGTGTAGCATGGAGCTGTGAGCGCCCGGGAGACCTTCCCTCTTC 997
DB |||||
QY 490 CAGTCAAGTATGCTCTCTCAGCAGACTCTCTCAGCAACAAGATCAATTCAAGTCTTC 549
DB |||||
QY 998 TTCCGACCGTGGCCAGGACCGGTGTGAGTGTGAGCGCGCGCGGAGCTGCTGAGGAG 1057
DB |||||
QY 550 CTCGAAACCAATCCCAATGATGAGACCCAGGCCATGCCATGGCAGACATCATCGAGTAT 609
DB |||||
QY 1058 TTCCGCTGGAAGTGGCGCGCTTGGCGCGCAGCAGAGTACGGCGCGCAGGCGCTG 1117
DB |||||
QY 610 TTCCGCTGGAAGTGGTGGGCGCAATTCAGCTGATGAGACTATGGCGCGCGCGGAGT 669
DB |||||
QY 1118 AGCATCTTCTCGGCGCTTGGCGCGCAGCGCGCATCTGATCGCGCAGAGGGCTGTG 1177
DB |||||
QY 670 GAGAAATTCGAGAGGAAGTCTGAGAAAGGATATCTGATCGACTTCAGTGAATCATC 729
DB |||||
QY 1178 CCGTGGCGCTGGCGGAGTACTCGGGTGGGAGGTGAGGAGTCTGACACCGAGG 1237
DB |||||
QY 730 TCCAGTACTCTGATGA-----GGAAGAGATCCAGCATGTGTAGAGTGAT 777
DB |||||
QY 1238 AACAGAGCAGGTGAGTGGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1297
DB |||||
QY 778 CAAATTCACGGCCAAAGTATCATCGTGTGTTTCTCCAGTGGCCCGCAGATCTTGAGCCCTC 837
DB |||||


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; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3809 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 373..3606
; OTHER INFORMATION:
;
US-08-485-568-3

Query Match 3.1%; Score 111; DB 1; Length 3809;
Best Local Similarity 51.7%; Pred. No. 5.4e-13;
Matches 286; Conservative 0; Mismatches 255; Indels 12; Gaps 1;

QY 938 CAGTCTGAGTACGCTGTAGTGGAGTGTGAGCGCGCGGAGAGCTTCCCTCTCTTC 997
Db 862 CAGTCTGAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 921
QY 998 TTCGCGACCGTCCCGACGCGCGTGTGAGTGTGAGCGCGCGCGGAGCTCTCAGAG 1057
Db 922 CTCGACACCATCCCAATGATGAGCACCAGCGCACTGCCATGGCAGACATCATGAT 981
QY 1058 TTCGCGTGAAGTGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1117
Db 982 TTCGCGTGAAGTGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1041
QY 1118 AGCATCTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1177
Db 1042 GAGAAATTCGAGAGGAGCTGAGGAGGAGGATATCTGCATCGACTTCAGTGAATCAT 1101
QY 1178 CCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1237
Db 1102 TCCAGTACTCTGATG-----GGAAGGATCCAGCATGTGTAGAGGTGATT 1149
QY 1238 AACAGAGACGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1297
Db 1150 CAAATTCACGGCGCAATATACGGGCAAGATCTGCTGGCGCAGCGAGCGCTGG 1209
QY 1298 TTCAACTACAGCATCAGCAGCAGCTCTCGCCCGAGGTGTGGTGGCGCAGCGCGCTGG 1357
Db 1210 ATCAAGAGATGTTCGGCGCAATATACGGGCAAGATCTGCTGGCGCAGCGAGCGCTGG 1269
QY 1358 CTGACCTCTGAGTGGTGTGAGTGGTGTGAGTGGTGTGAGTGGTGTGAGTGGTGTG 1417
Db 1270 GCCAGCTCTCTCTGATCGCATGCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1329
QY 1418 TTCCTCCAGAGGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1477

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Db 1330 TTCGCTCTGAAGGCTGGCGAGATCCCGAGGCTTCGGGAATTCTCTGAAGAGGTCCATCCC 1389
QY 1478 CTGCGCCACCGACC 1490
Db 1390 AGGAAGTCTGTCC 1402

RESULT 12
US-08-484-565-3
; Sequence 3, Application US/08484565
; Patent No. 5763569
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,565
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 955-0440
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3809 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA

```


Db 1102 TCCAGTACTCTGATGA-----GGAAGAGATCCAGCATGTGGTAGAGGTGATT 1149
 Qy 1238 AACAGAGAGCGTGCAGGTGGTCTGCTGTTCGCTCCGCTGCGTGCACGCGCCGCGCTC 1297
 Db 1150 CAAATTCACGCGCAAGTCATCGTGGTTTCTCCAGTGGCCGAGATCTTGAGCCCTC 1209
 Qy 1298 TTCAACTACAGCATCAGCAGGAGCTCTCGCCCAAGGTGTGGTGGCCAGCAGGCGCTGG 1357
 Db 1210 ATCAAGAGAGATTGTCCGCGCAATATCACGGGCAAGATCTGGTGGCCAGGAGCGCTGG 1269
 Qy 1358 CTGACCTCTGACCTGTGATGGGCTCGCGGCTCGCGGCAAGTGGCCAGATGGGCAAGTGGCTGGC 1417
 Db 1270 GCCAGCTCTCTCTGATCGCATGCTCCTCAGTACTTCCACGCTGGTGGCGGCAACATTTGA 1329
 Qy 1418 TTCTCTCAGAGGGTGGCCAGTCTCAGAGTTCCTCCAGTTCCTCCGGAATTCCTGAAGAGGTCCATCCC 1477
 Db 1330 TTCTCTGAGAGGTGGGAGATCCAGGCTTCCGGAATTCCTGAAGAGGTCCATCCC 1389
 Qy 1478 CTGCCACCGACC 1490
 Db 1390 AGGAAGTCTGTCC 1402

RESULT 14
 US-08-943-986-3
 ; Sequence 3, Application US/08943986
 ; Patent No. 5962314

GENERAL INFORMATION:
 APPLICANT: Edward M. Brown
 APPLICANT: Steven C. Hebert
 APPLICANT: James E. Garrett, Jr.
 TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
 TITLE OF INVENTION: MOLECULES
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: First Interstate World Center
 STREET: Suite 4700
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: FASTSEQ
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/943,986
 FILING DATE: 03-OCT-1997
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/484,565
 FILING DATE: 7-June-1995
 APPLICATION NUMBER: 08/353,784
 FILING DATE: 9 December, 1994
 APPLICATION NUMBER: PCN/US/94/12117
 FILING DATE: 21 October, 1994
 APPLICATION NUMBER: U.S. 08/292,827
 FILING DATE: 23 August, 1994
 APPLICATION NUMBER: U.S. 08/141,248
 FILING DATE: 22 October, 1993
 APPLICATION NUMBER: U.S. 08/009,389
 FILING DATE: 23 February, 1993
 APPLICATION NUMBER: U.S. 08/017,127
 FILING DATE: 12 February, 1993
 APPLICATION NUMBER: U.S. 07/934,161
 FILING DATE: 21 August, 1992
 APPLICATION NUMBER: U.S. 07/834,044
 FILING DATE: 11 February, 1992
 APPLICATION NUMBER: U.S. 07/749,451
 FILING DATE: 23 August, 1991

ATTORNEY/AGENT INFORMATION:
 NAME: Heber, Sheldon O.
 REGISTRATION NUMBER: 38,179
 REFERENCE/DOCKET NUMBER: 213/006
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3809 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 373..3606
 OTHER INFORMATION:
 US-08-943-986-3

Query Match 3.1%; Score 111; DB 2; Length 3809;
 Best Local Similarity 51.7%; Pred. No. 5.4e-13;
 Matches 286; Conservative 0; Mismatches 255; Indels 12; Gaps 1;

Qy 938 CAGGTACAGTACGCTGCTAGCATGGAGCTGCTGAGCGCCCGGAGACCTTCCCTCCTTC 997
 Db 862 CAGTCAAGTTATGCTCTCTCCAGCAGACTCTCAGCAACAAGAATCAATTTCAAGTCTTC 921
 Qy 998 TTCCGACCGTCCAGCAGCGGTGTGACGTGACGCGCCCGGAGAGCTTCCCTCCTTC 1057
 Db 922 CTCGACCATCTCCCAATGATGAGCACACGAGGATGCTGAGGATCATCGAGTAT 981
 Qy 1058 TTCCGCTGGAACCTGGGTGGCGCCCTCGGCGAGGACGACGAGTACGCGCGGAGGCTG 1117
 Db 982 TTCCGCTGGAACCTGGGTGGCGCAATTTGACGTGATGACGATATGAGGCGCGGAGT 1041
 Qy 1118 AGCATCTTCTCGGCCCTGGCGCGCATCTGATCGCGCATCTGCGCGACGAGGCGCTG 1177
 Db 1042 GAGAAATTCGAGAGAGGAGCTGAGGAAGGATATCTGCATCGACTTCAGTGAATCATC 1101
 Qy 1178 CCGTGCCTCGTCCGATGACTGCGGCTGGGAGAGTGTGAGGAGTCTGACAGGTC 1237
 Db 1102 TCCAGTACTCTGATGA-----GGAAGAGATCCAGCATGTGGTAGAGTATT 1149
 Qy 1238 AACAGAGAGCTGCGAGGTGGTGTGCTGCTGTTCCTCCGTCGACGCGCCGCGCTC 1297
 Db 1150 CAAATTCACGCGCAAGTCATCGTGGTTTCTCCAGTGGCCAGATCTTGAGCCCTC 1209
 Qy 1298 TTCAACTACAGCATCAGCAGGAGCTCTCGCCCAAGGTGTGGTGGCCAGCAGGCGCTGG 1357
 Db 1210 ATCAAGAGAGATTGTCCGCGCAATATCACGGGCAAGATCTGGTGGCCAGGAGCGCTGG 1269
 Qy 1358 CTGACCTCTGACCTGTGATGGGCTCGCGGCTCGCGGCAAGTGGCCAGATGGGCAAGTGGC 1417
 Db 1270 GCCAGCTCTCTCTGATCGCATGCTCCTCAGTACTTCCACGCTGGTGGCGGCAACATTTGA 1329
 Qy 1418 TTCTCTCAGAGGGTGGCCAGTGTGACGAGTTCCTCCAGTACGCTGAAGAGCGACCTGGCC 1477
 Db 1330 TTCTCTGAGAGGTGGGAGATCCAGGCTTCCGGAATTCCTGAAGAGGTCCATCCC 1389
 Qy 1478 CTGCCACCGACC 1490
 Db 1390 AGGAAGTCTGTCC 1402

RESULT 15
 US-08-353-784-3
 ; Sequence 3, Application US/08353784
 ; Patent No. 6011068
 ; GENERAL INFORMATION:
 APPLICANT: Edward F. Nemeth, Edward M.
 APPLICANT: Brown, Steven C. Hebert,

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 30, 2004, 13:37:08 ; Search time 157 Seconds
(without alignments)
1917.031 Million cell updates/sec

Title: US-10-035-045-21

Perfect score: 4443

Sequence: 1 MGPRKATICSFLFLWLAE.....ERNTPAVFNSMIQGYTMRD 839

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	4443	100.0	839	5	ABB79834 Human tas
2	4443	100.0	839	6	ABP70450 Amino aci
3	4443	100.0	839	8	ADG73580 Human T1R
4	4422	99.5	839	6	ABR43488 Human swe
5	4322.5	98.9	838	7	ADK90719 Human tas
6	3463.5	78.0	669	3	RAY77558 Human GPC
7	3463.5	78.0	669	6	ABP81755 Human G p
8	3231	72.7	843	3	RAY77556 Rat GPCR-
9	3231	72.7	843	6	ABR43494 Rat sweet
10	3231	72.7	843	7	ADK90717 Rat taste
11	3231	72.7	843	8	ADI41010 Rat taste
12	3231	72.7	843	8	ADI40978 Rat taste
13	3179	71.6	843	3	RAY77557 Mouse GPC
14	3179	71.6	843	7	ADK90718 Mouse tas
15	3179	71.6	843	8	ADM42817 Murine ta
16	3179	71.6	843	8	ADP70073 Mouse T1R
17	2532.5	57.0	661	6	ABR43491 Rat sweet
18	1456.5	32.8	840	3	RAY45021 Rat senso
19	1456.5	32.8	840	6	ABR43493 Rat sweet
20	1456.5	32.8	840	7	ADK90711 Rat taste
21	1456.5	32.8	840	7	ADJ93197 Rat taste
22	1456.5	32.8	840	8	ADI40979 Rat taste
23	1456.5	32.8	840	8	ADI41009 Rat taste
24	1455.5	32.8	840	3	RAY45028 Rat senso
25	1454.5	32.7	840	3	RAY45026 Rat senso

26	1453.5	32.7	840	3	RAY45027	AAV45027 Rat senso
27	1446.5	32.6	842	8	ADI40975	ADI40975 Mouse swe
28	1446.5	32.6	842	8	ADI41007	ADI41007 Mouse swe
29	1440.5	32.4	842	3	RAY45022	RAY45022 Mouse sen
30	1440.5	32.4	842	6	ABR43490	ABR43490 Mouse tas
31	1440.5	32.4	842	7	ADK90712	ADK90712 Mouse tas
32	1440.5	32.4	842	8	ADM42819	ADM42819 Murine ta
33	1440.5	32.4	842	8	ADP70072	ADP70072 Mouse T1R
34	1437.5	32.4	842	8	ADI41008	ADI41008 Mouse swe
35	1351.5	30.4	841	4	AAE11969	AAE11969 Human nov
36	1351.5	30.4	841	4	AAE10372	AAE10372 Human tas
37	1351.5	30.4	841	5	ABB77319	ABB77319 Human G-p
38	1351.5	30.4	841	5	ABB79833	ABB79833 Human tas
39	1351.5	30.4	841	6	ABP70449	ABP70449 Amino aci
40	1351.5	30.4	841	7	ADK90736	ADK90736 Human tas
41	1351.5	30.4	841	8	ADG73579	ADG73579 Human T1R
42	1351.5	30.4	841	8	ADM42821	ADM42821 Human tas
43	1350.5	30.4	841	7	ADC26177	ADC26177 Human tas
44	1334	30.0	840	7	ADK90713	ADK90713 Human tas
45	1289	29.0	929	7	ADC86415	ADC86415 Human GPC

ALIGNMENTS

RESULT 1
ABB79834
ID ABB79834 standard; protein; 839 AA.
XX AC ABE79834;
XX AC

DT 25-NOV-2002 (first entry)

DE Human taste cell specific receptor hT1R2.

XX hT1R2; T1R2; T1R; G-protein coupled receptor; receptor; human; taste;
KW sweet.

XX Homo sapiens.

XX W0200264631-A2.

XX 22-AUG-2002.

XX 03-JAN-2002; 2002WO-US000198.

XX 03-JAN-2001; 2001US-0259227P.

XX 19-APR-2001; 2001US-0284547P.

XX (SENO-) SENOMYX INC.

XX Adler JE, Li X, Staszewski L, O'Connell S, Zozulya S;

XX WPI; 2002-666991/71.

XX N-PSDB; ABR84928.

XX Novel mammalian taste-cell specific G protein-coupled receptors active in taste signaling, useful for representing the perception of taste and for predicting the perception of taste in a mammal.

XX Claim 152; Page 90; 132pp; English.

XX The present sequence is the protein sequence of a novel human G-protein coupled receptor (GPCR), designated hT1R2, that is involved in sweet taste transduction. The invention provides a new family of taste cell-specific GPCRs, the T1Rs, active in taste perception. Genomic DNAs and cDNAs encoding the receptors are described, along with methods for isolating T1R genes and for isolating and expressing T1R polypeptides. Methods for representing taste perception of a particular taste stimulus in a mammal, including a human, are also described, as are methods for generating novel molecules or combinations of molecules that elicit a predetermined taste perception in a mammal, and methods for stimulating one or more tastes. Methods for stimulating or blocking taste perception

are also disclosed, as are methods of screening for modulators of these novel taste cell-specific GPCRs. Such modulators are useful for pharmacological, chemical and genetic modulation of taste signalling pathways. They can be used in the food or pharmaceutical industries to customize taste, e.g. to modulate the sweet tastes of foods or drugs. T1R proteins and polypeptides are useful for identifying taste cells present in the oral cavity, gastrointestinal epithelium and epiglottis. They may also serve as tools for the generation of taste topographic maps that elucidate the relationship between the taste cells of the tongue and taste sensory neurons leading to taste centres in the brain

XX SQ Sequence 839 AA;

Query Match 100.0%; Score 4443; DB 5; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGRPRTICSLFLLVLAEPANSDPYLPGDYLGLFSLHANMGIHNLFLQVPMCK	60
DB	1	MGRPRTICSLFLLVLAEPANSDPYLPGDYLGLFSLHANMGIHNLFLQVPMCK	60
QY	61	EYEVKIVGNLMQAMFAVEEINDDSLPGVLLGYEIVDVVCYISNNVQVLYFLAHEDN	120
DB	61	EYEVKIVGNLMQAMFAVEEINDDSLPGVLLGYEIVDVVCYISNNVQVLYFLAHEDN	120
QY	121	LLPIQEDYNSISRVAVIGPDNSESVMTVANFSLFLPQITYSAISDELDRKVRFPAL	180
DB	121	LLPIQEDYNSISRVAVIGPDNSESVMTVANFSLFLPQITYSAISDELDRKVRFPAL	180
QY	181	LRTTPSADHHEAVMQLMHLFRNWIIVLVSSDTYGRDNGQLLGERVARRDICIATQETL	240
DB	181	LRTTPSADHHEAVMQLMHLFRNWIIVLVSSDTYGRDNGQLLGERVARRDICIATQETL	240
QY	241	PTLQPNQNMISERQRLVITVDLQOSTARVVVVFSPDLTLXHFNEVLKQNTFTGAVWIA	300
DB	241	PTLQPNQNMISERQRLVITVDLQOSTARVVVVFSPDLTLXHFNEVLKQNTFTGAVWIA	300
QY	301	SESWAIDPVLHNLTELGLHGLTFLGITTQSVPIPGFSEFEWGPQAGPPPLSRYSQYTCN	360
DB	301	SESWAIDPVLHNLTELGLHGLTFLGITTQSVPIPGFSEFEWGPQAGPPPLSRYSQYTCN	360
QY	361	QECDCNCLNATLSENTILRISGERVYVSVAVAHALHSLGCDKSTCKRVVYVWQL	420
DB	361	QECDCNCLNATLSENTILRISGERVYVSVAVAHALHSLGCDKSTCKRVVYVWQL	420
QY	421	LEBIKVNFTLLDHQIFFDPQGVDAHLLEIVQWDRSQNPFQSVASYPLQRLKNIQD	480
DB	421	LEBIKVNFTLLDHQIFFDPQGVDAHLLEIVQWDRSQNPFQSVASYPLQRLKNIQD	480
QY	481	ISMHTVNTTIPMSCKRQSQGKKPVGHIHVCCEIDCLPGTFLNHTDEYECQACPN	540
DB	481	ISMHTVNTTIPMSCKRQSQGKKPVGHIHVCCEIDCLPGTFLNHTDEYECQACPN	540
QY	541	NEWSYQSETSCFKRQIVLEWHHEAPTAVALLAALGFLSTLAILVIFWRHFTPIVRSAG	600
DB	541	NEWSYQSETSCFKRQIVLEWHHEAPTAVALLAALGFLSTLAILVIFWRHFTPIVRSAG	600
QY	601	GPICFLMLTLLVAYVMVVPVYVGPVKVSTCLCRQALPPLCFTICISCIARSFQIVCAFK	660
DB	601	GPICFLMLTLLVAYVMVVPVYVGPVKVSTCLCRQALPPLCFTICISCIARSFQIVCAFK	660
QY	661	MASRFPRAYSWRYQGVYVSMAFITVLKMWIVVIGMLATGLSPTRTDDPKITIVSC	720
DB	661	MASRFPRAYSWRYQGVYVSMAFITVLKMWIVVIGMLATGLSPTRTDDPKITIVSC	720
QY	721	NPNYRSLFNSTLSDLLSVVGFSPFAYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM	780
DB	721	NPNYRSLFNSTLSDLLSVVGFSPFAYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM	780
QY	781	SAYSGVLVTVDLLVTLNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRD	839
DB	781	SAYSGVLVTVDLLVTLNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRD	839

RESULT 2

ABP70450

ID ABP70450 standard; protein; 839 AA.

XX AC ABP70450;

XX DT 22-APR-2003 (first entry)

XX DE Amino acid sequence of human T1R2.

XX KW T1 receptor; T1R3; G protein-coupled receptor; GPCR; T1R2; T1R3;

XX KW sweet taste stimuli; T1R2; umami taste stimuli; taste stimuli;

XX KW taste perception; taste sensation.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT Misc-difference 221

XX FT /note= "Gln encoded by AG"

XX PN WO2003001876-A2.

XX PD 09-JAN-2003.

XX PF 26-JUN-2002; 2002WO-US019970.

XX PR 26-JUN-2001; 2001US-0300434P.

XX PR 03-JUL-2001; 2001US-0089742P.

XX PR 13-JUL-2001; 2001US-0304749P.

XX PR 08-AUG-2001; 2001US-0310493P.

XX PR 21-NOV-2001; 2001US-0331771P.

XX PR 14-DEC-2001; 2001US-0339472P.

XX PR 03-JAN-2002; 2002US-00035045.

XX PR 15-APR-2002; 2002US-0372090P.

XX PR 22-APR-2002; 2002US-0374143P.

XX PA (SENO-) SENOMYX INC.

XX PI Zoller MT, Li X, Staszewski L, O'Connell S, Zozulya S, Adler JE;

XX PI Xu H, Echeverri F;

XX XX WPI; 2003-210181/20.

XX DR N-PSDB; AB268279.

XX PT New receptor that comprises T1R1 and/or T1R3 or T1R2 and/or T1R3

XX PT polypeptide and that specifically binds to and/or is activated by umami

XX PT or sweet taste stimuli, useful for identifying compounds that modulate

XX PT taste perception.

XX PS Example 1; Page 80; 135pp; English.

XX CC The present sequence represents a human T1 receptor designated T1R2. The

XX CC receptor is a G protein-coupled receptor (GPCR). T1R2 and T1R3 act in

XX CC combination to recognise sweet taste stimuli, while T1R2 and T1R3 act in

XX CC combination to recognise umami taste stimuli. The specification describes

XX CC different combinations of T1Rs, that when co-expressed, produce

XX CC functional taste receptors that respond to taste stimuli. The hetero-

XX CC oligomeric taste receptors of the invention are useful for identifying

XX CC compounds that modulate taste perception. They are also useful for

XX CC modifying taste sensation in an animal

XX SQ Sequence 839 AA;

Query Match 100.0%; Score 4443; DB 6; Length 839;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPRTICSLFLLVLAEPANSDPYLPGDYLGLFSLHANMGIHNLFLQVPMCK 60

DB 1 MGRPRTICSLFLLVLAEPANSDPYLPGDYLGLFSLHANMGIHNLFLQVPMCK 60

QY 61 EYEVKIVGNLMQAMFAVEEINDDSLPGVLLGYEIVDVVCYISNNVQVLYFLAHEDN 120

QY 181 LRTTPSADHVEAMVQLMLHFRWNIIIVLVSSDTYGRDNGQLLGERVARDICIAFOETL 240
 Db 181 LRTTPSADHVEAMVQLMLHFRWNIIIVLVSSDTYGRDNGQLLGERVARDICIAFOETL 240
 QY 241 PTLPQNQMTSEERQRLVITVDKLQOSTARVVVVFSPDLTLXHFNEVLKQNFAGVWIA 300
 Db 241 PTLPQNQMTSEERQRLVITVDKLQOSTARVVVVFSPDLTLXHFNEVLKQNFAGVWIA 300
 QY 301 SESWADPVLHNLTELGHGTFGLGTTQSVPIPGFSEFRWGQAGPPPLSRSTQSYTCN 360
 Db 301 SESWADPVLHNLTELGHGTFGLGTTQSVPIPGFSEFRWGQAGPPPLSRSTQSYTCN 360
 QY 361 QECNCLNATLSFNTILRLSGERVYVSVAVVAHALSLGCDKSTCTKRVVWPQL 420
 Db 361 QECNCLNATLSFNTILRLSGERVYVSVAVVAHALSLGCDKSTCTKRVVWPQL 420
 QY 421 LEEIKVNFLLDHOIFDFDQGVVVAHLEIVQWDRSQNPFSQVASYPLQRLKNIQD 480
 Db 421 LEEIKVNFLLDHOIFDFDQGVVVAHLEIVQWDRSQNPFSQVASYPLQRLKNIQD 480
 QY 481 ISWHTVNTIPMSKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYECQACPN 540
 Db 481 ISWHTVNTIPMSKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYECQACPN 540
 QY 541 NEWSQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQPIVRSAG 600
 Db 541 NEWSQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQPIVRSAG 600
 QY 601 GPMCFMLTLLVAYMVVVPVGPVKVSTCLCRQALPFLCFTICISCIASVRSQIVCAFK 660
 Db 601 GPMCFMLTLLVAYMVVVPVGPVKVSTCLCRQALPFLCFTICISCIASVRSQIVCAFK 660
 QY 661 MASRFPAYSVWRYQGPVYSMAFITVLKMWIVVIGMLATGLSTTRDDPKITIVSC 720
 Db 661 MASRFPAYSVWRYQGPVYSMAFITVLKMWIVVIGMLATGLSTTRDDPKITIVSC 720
 QY 721 NPYNRLNLTSLDLLSVVGFSAVMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780
 Db 721 NPYNRLNLTSLDLLSVVGFSAVMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780
 QY 781 SAYSGVLVITVDLVTNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRD 839
 Db 781 SAYSGVLVITVDLVTNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRD 839
 RESULT 4
 ABR43488
 ID ABR43488 standard; protein; 839 AA.
 AC ABR43488;
 DT 21-JUL-2003 (first entry)
 DE Human sweet taste receptor T1R2 protein SEQ ID NO:4.
 KW Human; sweet taste receptor; T1R1; T1R2; T1R3; gene therapy;
 KW tasting defect; taste discrimination; chromosome 1.
 XX Homo sapiens.
 OS WO2003025137-A2.
 PN 27-MAR-2003.
 PD 17-SEP-2002; 2002WO-US029449.
 PF 18-SEP-2001; 2001US-0323450P.
 XX (IRMI-) IBM LLC.
 PA (SCRI) SCRIPES RES INST.
 PI Liao J, Ding S, Schultz PG;
 XX

DR WPI; 2003-363139/34.
 DR N-PSDB; ACC69593.
 XX New human sweet receptor gene, useful for preparing a composition for
 PT treating tasting defects or for enhancing taste discrimination.
 XX Claim 1; Page 61; 80pp; English.
 XX The present invention describes human, mouse and rat sweet taste
 CC receptors T1R1, T1R2 and T1R3. Human sweet taste receptors are located on
 CC chromosome 1, and mouse sweet taste receptors are located on chromosome
 CC 4. The sweet taste receptors can be used in gene therapy. They can also
 CC be used for preparing a composition for treating tasting defects or for
 CC enhancing taste discrimination. The present sequence represents human
 CC T1R2, which is given in the exemplification of the present invention
 XX
 SQ Sequence 839 AA;
 Query Match 99.5%; Score 4422; DB 6; Length 839;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 834; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MGPRAKTICSLFLLVLAEPANSDPYLPDYLGLFSLHANMKGIHNLFLQVPMCK 60
 Db 1 MGPRAKTICSLFLLVLAEPANSDPYLPDYLGLFSLHANMKGIHNLFLQVPMCK 60
 QY 61 EYEVKVIYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQVLYFLAHEDN 120
 Db 61 EYEVKVIYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQVLYFLAHEDN 120
 QY 121 LLPIQEDYSNYSIRVAVIGPDNSSEVMTVANFSLFLPLQITYSALSDRLKVRFPAL 180
 Db 121 LLPIQEDYSNYSIRVAVIGPDNSSEVMTVANFSLFLPLQITYSALSDRLKVRFPAL 180
 QY 181 LRTTPSADHVEAMVQLMLHFRWNIIIVLVSSDTYGRDNGQLLGERVARDICIAFOETL 240
 Db 181 LRTTPSADHVEAMVQLMLHFRWNIIIVLVSSDTYGRDNGQLLGERVARDICIAFOETL 240
 QY 241 PTLPQNQMTSEERQRLVITVDKLQOSTARVVVVFSPDLTLXHFNEVLKQNFAGVWIA 300
 Db 241 PTLPQNQMTSEERQRLVITVDKLQOSTARVVVVFSPDLTLXHFNEVLKQNFAGVWIA 300
 QY 301 SESWADPVLHNLTELGHGTFGLGTTQSVPIPGFSEFRWGQAGPPPLSRSTQSYTCN 360
 Db 301 SESWADPVLHNLTELGHGTFGLGTTQSVPIPGFSEFRWGQAGPPPLSRSTQSYTCN 360
 QY 361 QECNCLNATLSFNTILRLSGERVYVSVAVVAHALSLGCDKSTCTKRVVWPQL 420
 Db 361 QECNCLNATLSFNTILRLSGERVYVSVAVVAHALSLGCDKSTCTKRVVWPQL 420
 QY 421 LEEIKVNFLLDHOIFDFDQGVVVAHLEIVQWDRSQNPFSQVASYPLQRLKNIQD 480
 Db 421 LEEIKVNFLLDHOIFDFDQGVVVAHLEIVQWDRSQNPFSQVASYPLQRLKNIQD 480
 QY 481 ISWHTVNTIPMSKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYECQACPN 540
 Db 481 ISWHTVNTIPMSKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYECQACPN 540
 QY 541 NEWSQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQPIVRSAG 600
 Db 541 NEWSQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQPIVRSAG 600
 QY 601 GPMCFMLTLLVAYMVVVPVGPVKVSTCLCRQALPFLCFTICISCIASVRSQIVCAFK 660
 Db 601 GPMCFMLTLLVAYMVVVPVGPVKVSTCLCRQALPFLCFTICISCIASVRSQIVCAFK 660
 QY 661 MASRFPAYSVWRYQGPVYSMAFITVLKMWIVVIGMLATGLSTTRDDPKITIVSC 720
 Db 661 MASRFPAYSVWRYQGPVYSMAFITVLKMWIVVIGMLATGLSTTRDDPKITIVSC 720
 QY 721 NPYNRLNLTSLDLLSVVGFSAVMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780
 Db 721 NPYNRLNLTSLDLLSVVGFSAVMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780

QY 781 SAYSGVLTVTVLLVTVLNLALSLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRD 839
 DB 781 SAYSGVLTVTVLLVTVLNLALSLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRD 839

RESULT 5
 ID ADK90719
 AC ADK90719 standard; protein; 838 AA.
 AC ADK90719;
 DT 06-MAY-2004 (first entry)
 DE Human taste receptor T1R2 protein.
 DE Human taste receptor T1R2 protein.
 KW gene therapy; taste receptor; T1R3; T1R1; T1R2; taste-induced behavior;
 KW taste topographic map; tongue; taste cell; taste sensory neuron;
 KW brain taste center.
 XX Homo sapiens.
 XX WO2003004992-A2.
 XX 16-JAN-2003.
 XX 03-JUL-2002; 2002WO-US021269.
 XX 03-JUL-2001; 2001US-0302898P.
 XX 10-AUG-2001; 2001US-00927315.
 XX 22-FEB-2002; 2002US-0358925P.
 XX (REGC) UNIV CALIFORNIA.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Zuker CS, Ryba NUP, Chandrashekar J, Hoon MA, Nelson GA, Zhang Y;
 XX WPI; 2003-210382/20.
 XX N-PSDB; ADK90722.
 XX New taste receptors comprising a T1R3 polypeptide and optionally a T1R1
 PT or T1R2 polypeptide, useful as probes for identifying taste cells, and in
 PT gene therapy for correcting acquired and inherited genetic defects.
 XX Claim 22; SEQ ID NO 9; 119pp; English.

CC The invention relates to a novel taste receptor comprising a T1R3
 CC polypeptide and optionally a T1R1 or T1R2 polypeptide. The nucleic acids
 CC and proteins encoding the receptors may be used as probes to identify
 CC taste cells or subsets of taste cells or to dissect taste-induced
 CC behaviors, and in the generation of taste topographic maps that elucidate
 CC the relationship between the taste cells of the tongue and taste sensory
 CC neurons leading to taste centers in the brain. Nucleic acids encoding T1R
 CC protein can be used with highly density oligonucleotide array technology
 CC to identify T1R protein, orthologs, alleles, conservatively modified
 CC variants, and polymorphic variants in this invention. The nucleic acids
 CC may be inserted into vectors for gene therapy correct acquired and
 CC inherited genetic defects and other diseases. Compositions may be
 CC administered to elicit a therapeutic response in the patient. Modulators
 CC of sweet and/or amino acid taste transduction are useful for
 CC pharmacological and genetic modulation of sweet and amino acid taste
 CC ligands, and in food and pharmaceutical industries to customize taste.
 CC This sequence corresponds to the human T1R2 protein.

XX Sequence 838 AA;
 XX Query Match 98.9%; Score 4392.5; DB 7; Length 838;
 XX Best Local Similarity 99.3%; Pred. No. 0;
 XX Matches 833; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 MGPRAKTICSLFLLVWLAEPANSDYLPDYLGLGLFSLHANNKGVHLNFIQVPMCK 60
 DB 1 MGPRAKTICSLFLLVWLAEPANSDYLPDYLGLGLFSLHANNKGVHLNFIQVPMCK 60

QY 61 EYEVKVGYNLMQAMRFAVEIRINDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHDN 120
 DB 61 EYEVKVGYNLMQAMRFAVEIRINDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHDN 120

QY 121 LLPIQEDYSNYSIRVAVIGPDNSESVMVTANFLSLFLLPQITTYSAISDELKDKVRFAL 180
 DB 121 LLPIQEDYSNYSIRVAVIGPDNSESVMVTANFLSLFLLPQITTYSAISDELKDKVRFAL 180

QY 181 LRTTPSADHVEAMVQLMLHFRWNIIIVLVSSDITYGRDNGQLLGERVARRDICIATQETL 240
 DB 181 LRTTPSADHVEAMVQLMLHFRWNIIIVLVSSDITYGRDNGQLLGERVARRDICIATQETL 240

QY 241 PTLQPNQMTSEERQRLVTIVDKLQOSTARVVVVFSPDLTYLHFFNEVLRFNGTAVWIA 300
 DB 241 PTLQPNQMTSEERQRLVTIVDKLQOSTARVVVVFSPDLTYLHFFNEVLRFNGTAVWIA 300

QY 301 SESWAIDPVLHNLTELGHGTFGLGTTIQSVPIPGSEFREGWPGAGPPPLSRTSQSYTCN 360
 DB 301 SESWAIDPVLHNLTELGHGTFGLGTTIQSVPIPGSEFREGWPGAGPPPLSRTSQSYTCN 360

QY 361 QECNCLNATLSFNTILRLSGERVVYVSAYVAHALHSLGCDKSTCTKRVVYPMQL 420
 DB 361 QECNCLNATLSFNTILRLSGERVVYVSAYVAHALHSLGCDKSTCTKRVVYPMQL 420

QY 421 LEEIWKVNFLLDHOIFEDPDQGDVALHLEIVQWOWDRSQNPFSQSVASYPLQROLKNIQD 480
 DB 421 LEEIWKVNFLLDHOIFEDPDQGDVALHLEIVQWOWDRSQNPFSQSVASYPLQROLKNIQD 480

QY 481 ISWHTVNTIPMSMCKSRQSGQKKPVGIHVCCFECIDCLPGTFLNHTEDYECCQACPN 540
 DB 481 ISWHTVNTIPMSMCKSRQSGQKKPVGIHVCCFECIDCLPGTFLNHTEDYECCQACPN 540

QY 541 NEWSYQSETSCFKQLVLEWHEAPTAVALLAALGFLSTLAILVIFWRHFQTFIVRSAG 600
 DB 541 NEWSYQSETSCFKQLVLEWHEAPTAVALLAALGFLSTLAILVIFWRHFQTFIVRSAG 600

QY 601 GPMCFMLTLILLVAYMVVVPVGGPKVSTCLCRQALFPLCFTICISCIANVSFOIVCAFK 660
 DB 601 GPMCFMLTLILLVAYMVVVPVGGPKVSTCLCRQALFPLCFTICISCIANVSFOIVCAFK 660

QY 661 MASFPFRAYSVMVRYQGPVYSMAFITVLKMWIVVIGMLATGLSPTTRDPPDKITIVSC 720
 DB 661 MASFPFRAYSVMVRYQGPVYSMAFITVLKMWIVVIGMLARPOS-HPRTDPPDKITIVSC 719

QY 721 NPVNSLLFNTSLDILLVGVGSFAYMGKELPTNYNEAKFITLSMTFYETSSVSLCTFM 780
 DB 720 NPVNSLLFNTSLDILLVGVGSFAYMGKELPTNYNEAKFITLSMTFYETSSVSLCTFM 779

QY 781 SAYSGVLTVTVLLVTVLNLALSLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRD 839
 DB 780 SAYSGVLTVTVLLVTVLNLALSLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRD 838

RESULT 6
 AAY77558
 ID AAY77558 standard; protein; 669 AA.
 AC AAY77558;
 XX 08-MAY-2000 (first entry)
 XX Human GPCR-B4 polypeptide.
 XX Sensory transduction G-protein coupled receptor; GPCR; GPCR-B4; human;
 KW taste transduction pathway; taste receptor; foliate; fungiform; food;
 KW circumvallate; taste signaling; pharmaceutical.
 OS Homo sapiens.
 XX WO200006593-A1.
 XX 10-FEB-2000.

XX 27-JUL-1999; 99WO-US017104.
 PF 28-JUL-1998; 98US-0095464P.
 XX 17-DEC-1998; 98US-0112747P.
 PR (REGC) UNIV CALIFORNIA.
 XX
 PI Zuker CS, Adler JE, Lindemeier J;
 XX WPI; 2000-195257/17.
 DR N-PSDB; AA258965.
 XX
 PT New isolated sensory transduction G-protein coupled receptor, useful for
 PT developing products for use in studying and modulating the taste
 PT transduction pathway and for generating taste topographic maps.
 XX
 PS Claim 22; Page 73; 76pp; English.
 XX
 CC The invention provides nucleic acids encoding rat, mouse and human
 CC sensory transduction G-protein coupled receptor (GPCR) polypeptides. The
 CC GPCR polypeptides are components of the taste transduction pathway. The
 CC nucleic acids can be used to identify taste cells and as tools for the
 CC generation of taste topographic maps that elucidate the relationship
 CC between the taste cells of the tongue and taste sensory neurons leading
 CC to taste centers in the brain. GPCR-B4 is useful as a nucleic acid probe
 CC for identifying subpopulations of taste receptor cells such as foliate,
 CC fungiform, and circumvallate taste receptor cells. The polypeptides can
 CC be used for identifying compounds that modulate sensory signaling in
 CC sensory cells. Such modulators of taste transduction are useful for
 CC pharmacological and genetic modulation of taste signaling pathways. These
 CC modulatory compounds can then be used in the food and pharmaceutical
 CC industries to customize taste. The present sequence represents a human
 CC GPCR-B4 polypeptide
 XX
 SQ Sequence 669 AA;
 Query Match 78.0%; Score 3463.5; DB 3; Length 669;
 Best Local Similarity 97.5%; Pred. No. 0;
 Matches 661; Conservative 1; Mismatches 7; Indels 9; Gaps 3;
 162 ITYSAISDELRLKVRFPALLRTTSPADHVEAMVQLMLHFRWNIIIVLVSSDTYGRDNGQ 221
 DB 1 ITYSAISDELRLKVRFPALLRTTSPADHVEAMVQLMLHFRWNIIIVLVSSDTYGRDNGQ 60
 222 LLSERVARRDICTAFQETLTLPQNQNTSEERQRLVTIYDKLQOSTARVVVFPDLTL 281
 DB 61 LLSERVARRDICTAFQETLTLPQNQNTSEERQRLVTIYDKLQOSTARVVVFPDLTL 120
 282 YHFFNEVLQNFTGAVWIAESWAIDPVLNLTGELHGLTFLGTTIQSVPIPGFSEPREW 341
 DB 121 YHFFNEVLQNFTGAVWIAESWAIDPVLNLTGELHGLTFLGTTIQSVPIPGFSEPREW 180
 342 GPQAGPPPLSRTSQSYTCNQCNDCLNATLSFNTILRLSGERVVYSVAVVAHALHS 401
 DB 181 GPQAGPPPLSRTSQSYTCNQCNDCLNATLSFNTILRLSGERVVYSVAVVAHALHS 240
 402 LLGCDKSTCKRVVYPMQLLEEIKVNFLLDQIFPDQGDVALHLEIVQWQDRSQNP 461
 DB 241 LLGCDKSTCKRVVYPMQLLEEIKVNFLLDQIFPDQGDVALHLEIVQWQDRSQNP 300
 462 FQSVASYPLQRLQKNTQDTSWHTVNTTIPMSCKSRCSQSKKPKVGIHVCCECDICL 521
 DB 301 FQSVASYPLQRLQKNTQDTSWHTVNTTIPMSCKSRCSQSKKPKVGIHVCCECDICL 359
 522 PGTFNHTDEYECQACPNNEWSQSTSCFKQLVPLEWHEAPTIAVALLAALGFTLSTL 581
 DB 360 PGTFNHTDEYECQACPNNEWSQSTSCFKQLVPLEWHEAPTIAVALLAALGFTLSTL 412
 582 AILVIFWRHFTPTVRSAGGPMCFMLTLILVAVMVVYVGVVPPKVTCLCRQALFPLCF 641
 DB 413 AILVIFWRHFTPTVRSAGGPMCFMLTLILVAVMVVYVGVVPPKVTCLCRQALFPLCF 472

QY 642 TICISCIATVRSFQIVCAFWASRFFPRAYSQVYVRYQGPYVSMATITVLKMWIVVIGMLATG 701
 DB 473 TICISCIATVRSFQIVCAFWASRFFPRAYSQVYVRYQGPYVSMATITVLKMWIVVIGMLARP 532
 QY 702 LSPTTRTDPPDKITIVSCNPNVRSNLLNTSLLDLSLVVSGFSFAYMGKELPTNYEAKF 761
 DB 533 QS-HPRTDPPDKITIVSCNPNVRSNLLNTSLLDLSLVVSGFSFAYMGKELPTNYEAKF 591
 QY 762 ITLSMTFYFTSSVSLCTFMSAYSGVLVTIVDLSLVVNLNLLAISLGYPGPKCYMILFYPER 821
 DB 592 ITLSMTFYFTSSVSLCTFMSAYSGVLVTIVDLSLVVNLNLLAISLGYPGPKCYMILFYPER 651
 QY 822 NTPAYENSMIQYTMERD 839
 DB 652 NTPAYENSMIQYTMERD 669
 RESULT 7
 ABP81755
 ID ABP81755 standard; protein; 669 AA.
 AC ABP81755;
 XX
 DT 04-MAR-2003 (first entry)
 XX
 DE Human G protein-coupled receptor GPCR-B4 protein SEQ ID NO:683.
 XX
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.
 XX
 OS Homo sapiens.
 XX
 XX WO200261087-A2.
 XX
 XX 08-AUG-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050107.
 XX
 PR 19-DEC-2000; 2000US-0257144P.
 XX
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
 XX Burmer GC, Roush CL, Brown JP;
 XX
 XX WPI; 2003-046718/04.
 XX
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 XX
 PS Disclosure; Fig 1; 523pp; English.
 XX
 CC The present invention describes antigenic peptides (I) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for

CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC osteoarthritis, bacterial, fungal, protozoan or viral infections,
CC inflammation, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
XX
SQ Sequence 669 AA;

Query Match 78.0%; Score 3463.5; DB 6; Length 669;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 661; Conservative 1; Mismatches 7; Indels 9; Gaps 3;
QY 162 ITYSALDELDRKVPALLRTPSADHHEAMVQMLHFRNWNIIIVLVSSDTYGRDNGQ 221
DB 1 ITYSALDELDRKVPALLRTPSADHHEAMVQMLHFRNWNIIIVLVSSDTYGRDNGQ 60
QY 222 LLGERVARRDICIATFQETLPTLPQNQNTSBERQLVTIVDKLQOSTARVVVVFSPDLTL 281
DB 61 LLGERVARRDICIATFQETLPTLPQNQNTSBERQLVTIVDKLQOSTARVVVVFSPDLTL 120
QY 282 YHFEVRLQNFAGVATASWALDPVHNLTELGHGTFGLGITIQSVPIPGSEFREW 341
DB 121 YHFEVRLQNFAGVATASWALDPVHNLTELGHGTFGLGITIQSVPIPGSEFREW 180
QY 342 GPQAGPPPLSTQSYTCNQECNCLNATLNTLRLSGRNVVSVYSAVAVAHLS 401
DB 181 GPQAGPPPLSTQSYTCNQECNCLNATLNTLRLSGRNVVSVYSAVAVAHLS 240
QY 402 LLGCDKSTCRKRVVPVQLLBEIKVNFLLDQHFDPQGDVALHLEIVQWDRSQNP 461
DB 241 LLGCDKSTCRKRVVPVQLLBEIKVNFLLDQHFDPQGDVALHLEIVQWDRSQNP 300
QY 462 FQSVASYPLQRLKNIODISHTVNTIPMSMCKRQSGOKKPKVGIHVCCFECIDCL 521
DB 301 FQSVASYPLQRLKNIK-TSLHTVNTIPMSMCKRQSGOKKPKVGIHVCCFECIDCL 359
QY 522 PGTFLNHTDEVEQACPNNSVQSETSCFKROLVFLWHEAPTIAVALLAALGFLSTL 581
DB 360 PGTFLNHT-CPNNNSVQSETSCFKROLVFLWHEAPTIAVALLAALGFLSTL 412
QY 582 AILVIFWRHFQTPIVRSAGGPMCFMLTLLVAVYVVPVYVGGPKVSTCLCRQALFPLCF 641
DB 413 AILVIFWRHFQTPIVRSAGGPMCFMLTLLVAVYVVPVYVGGPKVSTCLCRQALFPLCF 472
QY 642 TICISCIATVRSFQVCAFKASRPFRAYSVYWRVQGPVSMFATVLMQWIVWGLMATG 701
DB 473 TICISCIATVRSFQVCAFKASRPFRAYSVYWRVQGPVSMFATVLMQWIVWGLMATG 532
QY 702 LSPTRTDDPDKITIVSCNPNYNSLLFNTSLDLLSVGFSFAYMCKELPTYNNAKF 761
DB 533 QS-HPRTPDDPKITIVSCNPNYNSLLFNTSLDLLSVGFSFAYMCKELPTYNNAKF 591
QY 762 ILSMTFTYFTSSVSLCTFMSAYSGLVTIVDLLVTLNLLAISLGYPGKCYMLFYPER 821
DB 592 ILSMTFTYFTSSVSLCTFMSAYSGLVTIVDLLVTLNLLAISLGYPGKCYMLFYPER 651
QY 822 NTPAYFNSMIQYTWRRD 839
DB 652 NTPAYFNSMIQYTWRRD 669

RESULT 8
AAY77556
ID AAY77556 standard; protein; 843 AA.

XX AAY77556;
XX 08-MAY-2000 (first entry)
XX Rat GPCR-B4 polypeptide.
XX Sensory transduction G-protein coupled receptor; GPCR; GPCR-B4; rat;
XX taste transduction pathway; taste receptor; foliate; fungiform; food;
XX circumvallate; taste signaling; pharmaceutical.
XX Rattus sp.
XX WO200006593-A1.
XX 10-FEB-2000.
XX 27-JUL-1999; 99WO-US017104.
XX 28-JUL-1998; 98US-0095464P.
XX 17-DEC-1998; 98US-012747P.
XX (REGC) UNIV CALIFORNIA.
XX Zuker CS, Adler JE, Lindemeier J;
XX WPI; 2000-195257/17.
XX N-FSDB; AAZ58963.
XX New isolated sensory transduction G-protein coupled receptor, useful for
XX developing products for use in studying and modulating the taste
XX transduction pathway and for generating taste topographic maps.
XX Claim 22; Page 69; 76pp; English.
XX The invention provides nucleic acids encoding rat, mouse and human
XX sensory transduction G-protein coupled receptor (GPCR) polypeptides. The
XX GPCR polypeptides are components of the taste transduction pathway. The
XX nucleic acids can be used to identify taste cells and as tools for the
XX generation of taste topographic maps that elucidate the relationship
XX between the taste cells of the tongue and taste sensory neurons leading
XX to taste centers in the brain. GPCR-B4 is useful as a nucleic acid probe
XX for identifying subpopulations of taste receptor cells such as foliate,
XX fungiform, and circumvallate taste receptor cells. The polypeptides can
XX be used for identifying compounds that modulate sensory signaling in
XX sensory cells. Such modulators of taste transduction are useful for
XX pharmacological and genetic modulation of taste signaling pathways. These
XX modulatory compounds can then be used in the food and pharmaceutical
XX industries to customize taste. The present sequence represents a rat GPCR
XX -B4 polypeptide
XX
SQ Sequence 843 AA;

Query Match 72.7%; Score 3231; DB 3; Length 843;
Best Local Similarity 70.8%; Pred. No. 1.9e-299;
Matches 596; Conservative 109; Mismatches 133; Indels 4; Gaps 2;
QY 1 MGPRAKTICSLFLLWLAEP---AENSDFYLPDGLLGLFSLHANKGIVHLNFIQVP 57
DB 1 MGPOARTCLLSLLHLVLPKGLVENSDFHLAGDYLLGLFTLHANVKSISHLVQLVP 60
QY 58 MCKEYEVKVGYNLMQAMRFAVEINNDSSLLPGVLLGYEIVDVYISNNVQPVLYFLAH 117
DB 61 KCNEFTMKVGYNLMQAMRFAVEINNCSSLLPGVLLGYEIVDVYISNNIHPLGLYFLAQ 120
QY 118 EDNLLPTQEDYSNYSIRVAVIGPDNSESVMTVANFLSLFLLPOITYSAISDELDRKVR 177
DB 121 DDDLLPLKDYQSYMPHVAVIGPDNSESITVSNILSHFLIPOITYSAISDELDRKVR 180
QY 178 PALLRTTPSADHHEAMVQMLHFRNWNIIIVLVSSDTYGRDNGQLLGERVAR-RDICIAT 236
DB 181 PSLMRTVPSATHIEAMVQMLWVHFQWNIIVLVVSDDDYGRNSHLLSRLTKTSDICIAF 240

QY 237 QETLPTLPONQNTSBERQRLVTIVDKLOOSTARVVVVVSPDLTYLHFFNEVLNQFTGA 296
 Db 241 QEVLPPIESSQVMSRSEQQLNDLRLRTSARVVVSPDLTYLHFFNEVLNQFTGA 300
 QY 297 VTIASWAIADPVLHNLTLGLHGTFLGTIGTQSVPIPGFSEFREWGPQAGPPPLSTQS 356
 Db 301 VTIASWAIADPVLHNLTLGLHGTFLGTIGTQSVPIPGFSEFREWGPQAGPPPLSTQS 360
 QY 357 YTCNQCDCLNATLSENTILRSGERVYVSVYSAVAHAHLHSLGCDKSTCTKRVVY 416
 Db 361 TTNQCDCLNATLSENTILRSGERVYVSVYSAVAHAHLHSLGCDKSTCTKRVVY 420
 QY 417 PWQLLEIKVNFLLDQIIFPDQGDVALLHLEIVQWDRSQNPQSVASVYPLQRLK 476
 Db 421 PWQLLEIKVNFLLDQIIFPDQGDVALLHLEIVQWDRSQNPQSVASVYPLQRLK 480
 QY 477 NIQDISHVNTIPMSCKRQSGQKQKPVGHVCCFECIDCLPGTFLNHTDEYECQ 536
 Db 481 YINNVSWYTPNNTVPVSMCKSKQCPQGMKKSGLHPCCFECIDCLPGTFLNHTDEYECQ 540
 QY 537 ACNNENWSQSETSCFKRLVLEWHEAPTIIVALLAALGFLSTLAILVFWRHFOPIV 596
 Db 541 SCFGSMWSYKNDITCFORRPTFLWHEVPTIVVAILAALGFFSTLAILVFWRHFOPIV 600
 QY 597 RSAGGPMCFMLTLVAVVMPVYVGPVKVSTCLCRQALFPLCFTICISCIARSQIV 656
 Db 601 RSAGGPMCFMLTLVAVVMPVYVGPVKVSTCLCRQALFPLCFTICISCIARSQIV 660
 QY 657 CAFKMASRFPRAVYVWYQGVYMAFIVLKWVIVIGMLATGLSTRTDPPDKIT 716
 Db 661 CVFKAARLPASVYFWNRHGVYVFAITAIKVALVGNMLATTINPIGRDTPDDNIM 720
 QY 717 IVSCNPNYRNSLLFNTSLDLLSVGFSFAYMGKELPTNYNEAKFTLSMTFTSSVSL 776
 Db 721 ILSCHPNYRNGLLFNTSMDLLSVLGSFAYMGKELPTNYNEAKFTLSMTFTSSVSL 780
 QY 777 CTWMSYGVIVTIVDLVTLNLAISLGYFGPKCYMILFYPERNTPAFNSMIQGYM 836
 Db 781 CTWMSYGVIVTIVDLVTLNLAISLGYFGPKCYMILFYPERNTPAFNSMIQGYM 840
 QY 837 RR 838
 Db 841 RK 842

RESULT 9

ABR43494
 ID ABR43494 standard; protein; 843 AA.

AC ABR43494;

DT 21-JUL-2003 (first entry)

DE Rat sweet taste receptor Tlr2 protein SEQ ID NO:6.

KW Rat; sweet taste receptor; Tlr1; Tlr2; Tlr3; gene therapy;
 KW tasting defect; taste discrimination.

OS Rattus sp.

PN WO2003025137-A2.

PD 27-MAR-2003.

PF 17-SEP-2002; 2002WO-US029449.

PR 18-SEP-2001; 2001US-0323450P.

PA (IRMI-) IRM LLC.

PA (SRI) SRIIPS RES INST.

PI Liao J, Ding S, Schultz PG;

XX

DR WPI; 2003-363139/34.
 XX N-PSDB; ACC69599.
 XX New human sweet receptor gene, useful for preparing a composition for
 PT treating tasting defects or for enhancing taste discrimination.
 XX Claim 1; Page 64; 80pp; English.
 XX The present invention describes human, mouse and rat sweet taste
 CC receptors Tlr1, Tlr2 and Tlr3. Human sweet taste receptors are located on
 CC chromosome 1, and mouse sweet taste receptors are located on chromosome
 CC 4. The sweet taste receptors can be used in gene therapy. They can also
 CC be used for preparing a composition for treating tasting defects or for
 CC enhancing taste discrimination. The present sequence represents rat Tlr2,
 CC which is given in the exemplification of the present invention

XX Sequence 843 AA;

Query Match 72.7%; Score 3231; DB 6; Length 843;
 Best Local Similarity 70.8%; Pred. No. 1.9e-299;
 Matches 596; Conservative 109; Mismatches 133; Indels 4; Gaps 2;

QY 1 MGPRATICSLPFLWLAEP---AENSDFPLPGDYLLGLGLSLHANMKGIVHLNLFQVP 57
 Db 1 MGPRATICSLPFLWLAEP---AENSDFPLPGDYLLGLGLSLHANMKGIVHLNLFQVP 60
 QY 58 MCKEYEVKIVGYNLMQAMRFAVEEINNDSLLPGVLLGYEIVDVCVISNNVQVPLXFLAH 117
 Db 61 KCEFTMKVGLYNLMQAMRFAVEEINNCSLLPGVLLGYEIVDVCVISNNVQVPLXFLAH 120
 QY 118 EDNLLPIQEDYSNIYISRVVAVIGPDNSSEVMVAVANFLSLPLLPQITYSAISDELKRVF 177
 Db 121 DDDLLPILKDYQYMPHVAVIGPDNSSEVMVAVANFLSLPLLPQITYSAISDELKRVF 180
 QY 178 PALLRTTPSADHVAWVQLMLHFRNWIIVLVSSDYGRDNGQLGGERVAR-RDICIAP 236
 Db 181 PSMRLTPSATHIEAMVQLMHFQWNIIVLVSDDDYGRNHLHSLGCDKSTCTKRVVY 240
 QY 237 QETLPTLPONQNTSBERQRLVTIVDKLOOSTARVVVVVSPDLTYLHFFNEVLNQFTGA 296
 Db 241 QEVLPPIESSQVMSRSEQQLNDLRLRTSARVVVSPDLTYLHFFNEVLNQFTGA 300
 QY 297 VTIASWAIADPVLHNLTLGLHGTFLGTIGTQSVPIPGFSEFREWGPQAGPPPLSTQS 356
 Db 301 VTIASWAIADPVLHNLTLGLHGTFLGTIGTQSVPIPGFSEFREWGPQAGPPPLSTQS 360
 QY 357 YTCNQCDCLNATLSENTILRSGERVYVSVYSAVAHAHLHSLGCDKSTCTKRVVY 416
 Db 361 TTNQCDCLNATLSENTILRSGERVYVSVYSAVAHAHLHSLGCDKSTCTKRVVY 420
 QY 417 PWQLLEIKVNFLLDQIIFPDQGDVALLHLEIVQWDRSQNPQSVASVYPLQRLK 476
 Db 421 PWQLLEIKVNFLLDQIIFPDQGDVALLHLEIVQWDRSQNPQSVASVYPLQRLK 480
 QY 477 NIQDISHVNTIPMSCKRQSGQKQKPVGHVCCFECIDCLPGTFLNHTDEYECQ 536
 Db 481 YINNVSWYTPNNTVPVSMCKSKQCPQGMKKSGLHPCCFECIDCLPGTFLNHTDEYECQ 540
 QY 537 ACNNENWSQSETSCFKRLVLEWHEAPTIIVALLAALGFLSTLAILVFWRHFOPIV 596
 Db 541 SCFGSMWSYKNDITCFORRPTFLWHEVPTIVVAILAALGFFSTLAILVFWRHFOPIV 600
 QY 597 RSAGGPMCFMLTLVAVVMPVYVGPVKVSTCLCRQALFPLCFTICISCIARSQIV 656
 Db 601 RSAGGPMCFMLTLVAVVMPVYVGPVKVSTCLCRQALFPLCFTICISCIARSQIV 660
 QY 657 CAFKMASRFPRAVYVWYQGVYMAFIVLKWVIVIGMLATGLSTRTDPPDKIT 716
 Db 661 CVFKAARLPASVYFWNRHGVYVFAITAIKVALVGNMLATTINPIGRDTPDDNIM 720
 QY 717 IVSCNPNYRNSLLFNTSLDLLSVGFSFAYMGKELPTNYNEAKFTLSMTFTSSVSL 776
 Db 721 ILSCHPNYRNGLLFNTSMDLLSVLGSFAYMGKELPTNYNEAKFTLSMTFTSSVSL 780

QY 777 CTFSAYSGVLVTIVDLVTVLNLIAISLGYFGPKCYMILFYPERNTPAYFNMSIQGYTM 836
 DB 781 CTFSVHDGVLVTIMDLVTVLNLIAISLGYFGPKCYMILFYPERNTSAYFNMSIQGYTM 840

QY 837 RR 838
 DB 841 RK 842

RESULT 10
 ID ADK90717 standard; protein; 843 AA.
 AC
 AC
 DT 06-MAY-2004 (first entry)
 XX
 XX Rat taste receptor Tlr2 protein.
 XX gene therapy; taste receptor; Tlr3; Tlr1; Tlr2; taste-induced behavior;
 KW taste topographic map; tongue; taste cell; taste sensory neuron;
 KW brain taste center.
 XX
 OS Rattus sp.
 XX
 XX WO2003004992-A2.
 XX
 PD 16-JAN-2003.
 XX
 XX 03-JUL-2002; 2002WO-US021269.
 XX
 XX 03-JUL-2001; 2001US-0302898P.
 PR 10-AUG-2001; 2001US-00927315.
 PR 22-FEB-2002; 2002US-0358925P.
 XX
 XX (REGC) UNIV CALIFORNIA.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Zuker CS, Ryba NJP, Chandrashekar J, Hoon MA, Nelson GA, Zhang Y;
 PI
 XX
 DR WPI; 2003-210382/20.
 DR N-PSDB; ADK90720.
 XX
 PT New taste receptors comprising a Tlr3 polypeptide and optionally a Tlr1
 or Tlr2 polypeptide, useful as probes for identifying taste cells, and in
 PT gene therapy for correcting acquired and inherited genetic defects.
 XX
 PS Claim 22; SEQ ID NO 7; 119pp; English.

XX The invention relates to a novel taste receptor comprising a Tlr3
 CC polypeptide and optionally a Tlr1 or Tlr2 polypeptide. The nucleic acids
 CC and proteins encoding the receptors may be used as probes to identify
 CC taste cells or subsets of taste cells or to dissect taste-induced
 CC behaviors, and in the generation of taste topographic maps that elucidate
 CC the relationship between the taste cells of the tongue and taste sensory
 CC neurons leading to taste centers in the brain. Nucleic acids encoding Tlr
 CC protein can be used with highly density oligonucleotide array technology
 CC to identify Tlr protein, orthologs, alleles, conservatively modified
 CC variants, and polymorphic variants in this invention. The nucleic acids
 CC may be inserted into vectors for gene therapy correct acquired and
 CC inherited genetic defects and other diseases. Compositions may be
 CC administered to elicit a therapeutic response in the patient. Modulators
 CC of sweet and/or amino acid taste transduction are useful for
 CC pharmacological and genetic modulation of sweet and amino acid taste
 CC ligands, and in food and pharmaceutical industries to customize taste.
 CC This sequence corresponds to the rat Tlr2 protein.

XX Sequence 843 AA;

Query Match 72.7%; Score 3231; DB 7; Length 843;
 Best Local Similarity 70.8%; Pred. No. 1.9e-299;
 Matches 596; Conservative 109; Mismatches 133; Indels 4; Gaps 2;

QY 1 MGPRAKTICSLFFLLWLAEPP--AENSDFYLPDGYLLGGFLSLHANNKMGVHLNLFLOVP 57
 DB 1 MGPOARTICLLSLLHLVLPKPKGLVENSDFHAGDYLLGGFLTHANNKVSISHLSYLOVP 60

QY 58 MKEYEYKVGYNLMQAMRFAVEEINNDSLSLPGVLLGYEIVDVCYISNNYQPVLYFLAH 117
 DB 61 KCNEFTMKVLGYNLMQAMRFAVEEINNCSLSLPGVLLGYEMVDVCYLSNNHHPGLYFLAQ 120

QY 118 EDNLLPIQEDYSNYISRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELRDKVRF 177
 DB 121 DDDLLPILKDYQSYMPHVAVIGPDNSESATVSNILSHFLIPQITYSAISDKLRDKRHF 180

QY 178 PALLRTTPSADHVEAMVQLMLHFRNWIIVLVSSDYGRDNGOLLGERVAR-RDICTAF 236
 DB 181 PSLRTVPSATHHEAMVQLMVFHFWNWIIVLVSSDDYGRNSHLLSQRLLTKTSDICTAF 240

QY 237 QETLPTLQPNQNTSEERQLVTIVDKLOOSTARVVVVVFPDLTYLHFFNEVLQNFTGA 296
 DB 241 QEVLPPESSQVMESEQRQLDNILKLRTSARVVVVVFPSELSLYSFFHEVLWNFTGF 300

QY 297 VWIASESWAIDPVLHNLTELHGLTGLTIGTIOQVPIPGFSEFRWGPQAGPPPLSRTSQS 356
 DB 301 VWIASESWAIDPVLHNLTELHGLTGLTIGTIOQVPIPGFSEFRWGPQAGPPPLSRTSQS 360

QY 357 YTCNOECDNCINATLSFNTILLSGERVYVYSAVVAHALHSLGLGCKSTCTKRVVY 416
 DB 361 TTCNQDCDACLNTKSNFNNILLSGERVYVYSAVVAHALHRLGNCVRCTKQKVY 420

QY 417 PWOLLEIKVNFLLDHDQIFPDQGDVALHLEIVQWQDRSQNPFOVSASYYPQLQK 476
 DB 421 PWOLLEIKVNFLLDHDQIFPDQGDVALHLEIVQWQDRSQNPFOVSASYYPQLQK 480

QY 477 NIQDISWHTVNTTPMSMCKRQSQGKKPKVGIHVCCFECIDCLDGTFLNHTDEVEQC 536
 DB 481 YINNVSWYTNNTVPVSMCKSQCPQGMKKSVGLHPCCFECLDCMPGTYNRSADFNCL 540

QY 537 ACPNNEWSYOSETSCFKQLVFLBWEHAPTIAVALLAALGFLSLTALIVPWRHFQPIV 596
 DB 541 SCFQSMWSYKNDITCFQRRPTFLWHEVPTIVAVALLAALGFFSLALIFPWRHFQPIV 600

QY 597 RSAGGPMCFMLTLTLLVAYMVVPPVYVGPVKVSTCLCRQALFPLCFTICISCIARVSQIV 656
 DB 601 RSAGGPMCFMLTLLAFGMVPPVYVGPVTVVSCFCQAFVTVCFISCLSCITVRSQIV 660

QY 657 CAFQMASRFPKAYVWRYQGPVSMAFITVLMVIVIGMLATGLSPTRTDDPKIT 716
 DB 661 CVFQMARLFPKAYVWRYQGPVSMAFITVLMVIVIGMLATGLSPTRTDDPKIT 720

QY 717 IVSCNPNYRNSLLFNTSLDILLSVVGFSFAYMGKELPTNYNEAKFITLSMTFETSSVSL 776
 DB 721 ILSCHPNYRNGLLFNTSLDILLSVVGFSFAYMGKELPTNYNEAKFITLSMTFETSSVSL 780

QY 777 CTFSAYSGVLVTIVDLVTVLNLIAISLGYFGPKCYMILFYPERNTPAYFNMSIQGYTM 836
 DB 781 CTFSVHDGVLVTIMDLVTVLNLIAISLGYFGPKCYMILFYPERNTSAYFNMSIQGYTM 840

QY 837 RR 838
 DB 841 RK 842

RESULT 11
 ID ADI41010 standard; protein; 843 AA.
 XX
 AC ADI41010;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Rat taste receptor TR2 #2.
 XX
 KW Receptor; GPCR; G protein-coupled receptor; reproductive disorder;

KW testicular disorder; vas deferens disorder; spermatogenesis; infertility;
 KW XX male; epididymitis; cryptorchidism; sperm transport disorder;
 KW testicular cancer; testicular germ cell tumour; male hormone disorder;
 KW premature puberty; Kallman syndrome; Cushing's syndrome; immune disorder;
 KW leukemia; arthritis; asthma; AIDS; rheumatoid arthritis;
 KW inflammatory bowel disease; sepsis; T-cell mediated cytotoxicity;
 KW graft-versus-host disease; autoimmunity disorder;
 KW systemic lupus erythematosus; drug induced haemolytic anaemia;
 KW Sjogren's disease; T-cell maturation disorder;
 KW B-cell maturation disorder; vascular disorder; stroke; ischaemia;
 KW myocardial infarction; atherosclerosis; gastrointestinal disorder; ulcer;
 KW pulmonary disorder; brain disorder; endocrine disorder; cancer;
 KW gene therapy.
 XX Rattus norvegicus.
 OS
 XX
 XX US2004018976-A1.
 PN
 XX
 XX 29-JAN-2004.
 PD
 XX 13-MAY-2003; 2003US-00436715.
 PF
 XX 14-MAY-2002; 2002US-0380336P.
 PR
 XX (FEDE/) FEDER J N.
 PA (MINT/) MINTIER G.
 PA (RAMA/) RAMANATHAN C S.
 XX
 XX Feder JN, Mintier G, Ramanathan CS;
 PI
 XX WPI; 2004-122081/12.
 DR
 XX
 XX New human G-protein coupled receptor polypeptide and polynucleotide,
 PT useful for diagnosing, preventing, treating or ameliorating a medical
 PT condition, e.g. reproductive disorder, immunodeficiency disease or
 PT testicular cancer.
 PT
 XX
 XX Disclosure; SEQ ID NO 70; 290pp; English.
 PS
 XX
 XX The invention relates to an isolated human G protein-coupled receptor
 CC polypeptide and its encoding polynucleotide, including the full length
 CC proteins minus the start methionine (and the region of the polynucleotide
 CC encoding this protein region). The proteins are designated HGPBMY30-1,
 CC HGPBMY30-2, HGPBMY30-3, HGPBMY41-1, HGPBMY41-2, HGPBMY41-3,
 CC HGPBMY42, HGPBMY42-1, HGPBMY43 and HGPBMY44. Also included are
 CC expression vectors, host cells, antibodies, preventing (treating or
 CC ameliorating) a medical condition comprising administering to a mammalian
 CC subject the polypeptide or its modulator and diagnosing a pathological
 CC condition or a susceptibility to a pathological condition in a subject
 CC (comprising determining the presence or absence of a mutation in the
 CC polynucleotide, or the presence or amount of expression of the
 CC polypeptide in a biological sample and diagnosing a pathological
 CC condition or a susceptibility to a pathological condition based on the
 CC presence or absence of the mutation, or the presence or amount of
 CC expression of the polypeptide). The human G-protein coupled receptor
 CC polypeptide or polynucleotide can be used for diagnosing a pathological
 CC condition or a susceptibility to a pathological condition in a subject,
 CC and for preventing, treating or ameliorating a medical condition, such as
 CC a disorder related to aberrant G-protein coupled receptor activity, a
 CC disorder related to aberrant signal transduction, a reproductive disorder
 CC ; a male reproductive disorder, a testicular disorder, a vas deferens
 CC disorder, spermatogenesis, infertility, Klinefelter's syndrome, XX male,
 CC epididymitis, genital warts, germinal cell aplasia, cryptorchidism,
 CC varicocele, immotile cilia syndrome, viral orchitis, sperm transport
 CC disorders, testicular cancer, choriocarcinoma, non-seminoma, seminoma,
 CC testicular germ cell tumours, male hormone disorders, premature puberty,
 CC incomplete puberty, Kallman syndrome, Cushing's syndrome, an immune
 CC disorder, a proliferative immune disorder, leukaemia, arthritis, asthma,
 CC immunodeficiency diseases such as AIDS, rheumatoid arthritis,
 CC granulomatous disease, inflammatory bowel disease, sepsis, acne,
 CC neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell
 CC mediated cytotoxicity, immune reactions to transplanted organs and
 CC tissues, such as host-versus-graft and graft-versus-host diseases, or

CC autoimmunity disorders, such as autoimmune infertility, demyelination,
 CC systemic lupus erythematosus, drug induced haemolytic anaemia, Sjogren's
 CC disease, scleroderma, T-cell maturation disorders, B-cell maturation
 CC disorders, vascular disorders, stroke, ischaemia, myocardial infarction,
 CC atherosclerosis, embolisms, thrombosis, gastrointestinal disorders,
 CC irritable bowel syndrome, ulcers, pulmonary disorders, brain disorders,
 CC endocrine disorders, or ovarian, stomach, colon or kidney cancer or its
 CC related proliferative condition (many other diseases and disorders are
 CC listed in the specification). The antibodies may be used to purify,
 CC detect and target the G-protein coupled receptor polypeptides. The
 CC polynucleotides are also useful in gene therapy. The present sequence
 CC represents a species homologue of a novel GPCR of the invention.
 XX
 SQ Sequence 843 AA;
 Query Match 72.7%; Score 3231; DB 8; Length 843;
 Best Local Similarity 70.8%; Pred. No. 1.9e-299;
 Matches 596; Conservative 109; Mismatches 133; Indels 4; Gaps 2;
 QY 1 MGPRKATICSLEFLLWVLAEP---AENSDFYLPDGYLLGGLFSLHANMKGIHVHNFLOVP 57
 DB 1 MGFPARTCLLSLLHVLKPKGLVENSDFHLGADYLLGGLFTTHANVKSISHLSYLOVP 60
 QY 58 MCKEYEVKIVGYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDYCYISNNVQPVLYELAH 117
 DB 61 KCNEFTMKVLGVNLMQAMRFAVEEINNCSSLLPGVLLGYEMVDVCSLNNHFGVFLAQ 120
 QY 118 EDNLLPIQEDYSNIYISRVVAVIGPDNSVMTVANFLSLFLLPQITYSAISDELKDKVRF 177
 DB 121 DDLLLPILKDYQYMPHVAVIGPDNSESAITSNLSHFLIPQITYSAISDKLRKHF 180
 QY 178 PALLRTPSADHHEAVQMLHFRWNWIIIVSSDTYGRDNGQLGGERVAR-RDICIAP 236
 DB 181 PSLMRTVPSATHIEAMVQLVHFQWNWIIIVLSDDDYGRNSHLLSRLTSDICIAP 240
 QY 237 QETPLTLPQNQNTSEERQRLVTVDKLOQSTARVWVVFSPDITLHFNEVLQRNFTGA 296
 DB 241 QEVLPIPESSQVNRSEERQDLNLDKLRTSARVWVVFSPESLSYFFHEVLWRNFTGF 300
 QY 297 VTIASWSAIDPVLHNLTELGLTGLTIGTQVPIPGFSEFREWGPQAGPPPLSRTSQS 356
 DB 301 VTIASWSAIDPVLHNLTELHRTGTGLVTIQVRSVPGSFQVRVRDKPYVPNTNLR 360
 QY 357 YTCNQECDCNCLNATLSFNTILRLSGRVVSVYSAVAVAHLSLGCDSKSTCTKRVVY 416
 DB 361 TTCNQDCDACLNTKTSFNILILSGRVVSVYSAVAVAHLSLGCNRVCTKQKVY 420
 QY 417 PWQLLEIKVNTLIDHQIFPDQGDVALHLEIVQWQDRSONPQSVASYVPLQRLK 476
 DB 421 PWQLLEIKVNTLIDHQIFPDQGDVALHLEIVQWQDRSONPQSVASYVPLQRLK 480
 QY 477 NIQDIGHWTVNNTIPMSMCKSCQSGQKKKPVGHVCCPECIDCLPCTFLNHTDEYECQ 536
 DB 481 YINNVSWYPTNTPVSMCKSCQSGQKKKPVGHVCCPECIDCLPCTFLNHTDEYECQ 540
 QY 537 ACPNNEKSWQSESCPCQKQLVLEHBAPTIAVALAALGFLSTLAILVFWHRFQPIV 596
 DB 541 SCPSGMSKSNITCQRRPTFLEHEVPTIVVAIALAALGFLSTLAILVFWHRFQPMV 600
 QY 597 RSAGGPMCFMLTLVAVYVVPVYVPPKVSCLCQALFPLCFTICISIAVRSQIV 656
 DB 601 RSAGGPMCFMLVPLVLAAGVYVPPVYVPPVFCFCRQAFVTCFSLCISIAVRSQIV 660
 QY 657 CAFKMASRFPAYSVYVYQGPVSMATFVLKQVIVWIGMLATGLSPTRTDDPKIT 716
 DB 661 CVFKMARLPSAYSFWRYHGPVVFVAFITAIKVALVVGNNMLATTINPIGRTDDDDNIM 720
 QY 717 IVSCNPYRNLSLNTSLDLSLVGFSFAYMKGELPTNNYNEAKFITLSMTFTSSVSL 776
 DB 721 ILSCHPNYRNGLLNTSLDLSLVGFSFAYMKGELPTNNYNEAKFITLSMTFTSSISL 780
 QY 777 CTFMSYSGVLVITVLLVTVLNLAILSLGYFQPKCYMILFYPERNTPAYFNSMQVYM 836

Db 781 CTFMSVHDGVLTIMDLLVTLNLAIGLVGFGPKCYMILFYPERNTSAYFNSMIQGYTM 840

QY 837 RR 838

Db 841 RK 842

RESULT 12

ADI40978

XX ADI40978 standard; protein; 843 AA.

AC ADI40978;

XX 22-APR-2004 (first entry)

DT

DE Rat taste receptor TR2.

XX

XX Receptor; GPCR; G protein-coupled receptor; reproductive disorder;

KW testicular disorder; vas deferens disorder; spermatogenesis; infertility;

KW XX male; epididymitis; cryptorchidism; sperm transport disorder;

KW testicular cancer; testicular germ cell tumour; male hormone disorder;

KW premature puberty; Kallman syndrome; Cushing's syndrome; immune disorder;

KW leukaemia; arthritis; asthma; AIDS; rheumatoid arthritis;

KW inflammatory bowel disease; sepsis; T-cell mediated cytotoxicity;

KW graft-versus-host disease; autoimmunity disorder;

KW Sjogren's disease; T-cell maturation disorder;

KW B-cell maturation disorder; vascular disorder; stroke; ischaemia;

KW myocardial infarction; atherosclerosis; gastrointestinal disorder; ulcer;

KW pulmonary disorder; brain disorder; endocrine disorder; cancer;

KW gene therapy.

XX

OS Rattus norvegicus.

XX

FN US2004018976-A1.

XX

PD 29-JAN-2004.

XX

PF 13-MAY-2003; 2003US-00436715.

XX

PR 14-MAY-2002; 2002US-0380336P.

XX

PA (FEDE/) FEDER J N.

PA (MINT/) MINTIER G.

PA (RAMA/) RAMANATHAN C S.

XX

XX Feder JN, Mintier G, Ramanathan CS;

PI

XX WPI; 2004-122081/12.

DR

XX New human G-protein coupled receptor polypeptide and polynucleotide,

PT useful for diagnosing, preventing, treating or ameliorating a medical

PT condition, e.g. reproductive disorder, immunodeficiency disease or

PT testicular cancer.

XX

FS Disclosure; SEQ ID NO 38; 290pp; English.

XX

CC The invention relates to an isolated human G protein-coupled receptor

CC polypeptide and its encoding polynucleotide, including the full length

CC proteins minus the start methionine (and the region of the polynucleotide

CC encoding this protein region). The proteins are designated HGPBMY30-1,

CC HGPBMY30-2, HGPBMY30-3, HGPBMY41-1, HGPBMY41-2, HGPBMY41-3,

CC HGPBMY42, HGPBMY42-1, HGPBMY43 and HGPBMY44. Also included are

CC expression vectors, host cells, antibodies, preventing (treating or

CC ameliorating) a medical condition comprising administering to a mammalian

CC subject the polypeptide or its modulator and diagnosing a pathological

CC condition or a susceptibility to a pathological condition in a subject

CC (comprising determining the presence or absence of a mutation in the

CC polynucleotide, or the presence or amount of expression of the

CC polypeptide in a biological sample and diagnosing a pathological

CC condition or a susceptibility to a pathological condition based on the

CC presence or absence of the mutation, or the presence or amount of

CC expression of the polypeptide). The human G-protein coupled receptor

CC polypeptide or polynucleotide can be used for diagnosing a pathological

CC condition or a susceptibility to a pathological condition in a subject,

CC and for preventing, treating or ameliorating a medical condition, such as

CC a disorder related to aberrant signal transduction, a reproductive disorder

CC ; a male reproductive disorder, a testicular disorder, a vas deferens

CC disorder, spermatogenesis, infertility, Klinefelter's syndrome, XX male,

CC epididymitis, genital warts, germinal cell aplasia, cryptorchidism,

CC varicocele, motile cilia syndrome, viral orchitis, sperm transport

CC disorders, testicular cancer, choriocarcinoma, non-seminoma, seminoma,

CC testicular germ cell tumours, male hormone disorders, premature puberty,

CC incomplete puberty, Kallman syndrome, Cushing's syndrome, an immune

CC disorder, a proliferative immune disorder, leukaemia, arthritis, asthma,

CC immunodeficiency diseases such as AIDS, rheumatoid arthritis,

CC granulomatous disease, inflammatory bowel disease, sepsis, acne,

CC neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell

CC mediated cytotoxicity, immune reactions to transplanted organs and

CC tissues, such as host-versus-graft and graft-versus-host diseases, or

CC autoimmunity disorders, such as autoimmune infertility, demyelination,

CC systemic lupus erythematosus, drug induced haemolytic anaemia, Sjogren's

CC disease, scleroderma, T-cell maturation disorders, B-cell maturation

CC disorders, vascular disorders, stroke, ischaemia, myocardial infarction,

CC atherosclerosis, embolisms, thrombosis, gastrointestinal disorders,

CC irritable bowel syndrome, ulcers, pulmonary disorders, brain disorders,

CC endocrine disorders, or ovarian, stomach, colon or kidney cancer or its

CC related proliferative condition (many other diseases and disorders are

CC listed in the specification). The antibodies may be used to purify,

CC detect and target the G-protein coupled receptor polypeptides. The

CC polynucleotides are also useful in gene therapy. The present sequence

CC represents a species homologue of a novel GPCR of the invention.

XX

QY Sequence 843 AA;

Query Match 72.7%; Score 3231; DB 8; Length 843;

Best Local Similarity 70.8%; Pred. No. 1.9e-299;

Matches 596; Conservative 109; Mismatches 133; Indels 4; Gaps 2;

QY 1 MGPRAKTICSLFLLWLAEP---AENSDFVLPDGLGLGFLSHANNKGVHNLFLQVP 57

Db 1 MGPOARTICLLSLHLVLPKPKLVENSDFHLAGDYLGLGLTHANNKVSLSHLYQVP 60

QY 58 MCKEYEVKVGYNLMQAMRFAVEEINDDSLPGVLLGYEIVDVCYISNNQPVLYFLAH 117

Db 61 KCNEFTMKVLGYNLMQAMRFAVEEINDDSLPGVLLGYEIVDVCYISNNHPIGLYFLAQ 120

QY 118 EDNLPTQEDYSNYSIRVAVIGPDNSESMTVANFLSLFLLPQITYSASIDELDKVRF 177

Db 121 DDDLLPILKQYSQYMPHVAVIGPDNSESMTVANFLSLFLLPQITYSASIDELDKVRF 180

QY 178 FALLRTTSDADHVEAMVQLMHLFERNWIIIVLSSDTYGRDNGOLLGERVAR-RDICIAP 236

Db 181 PSLMRTVPSATHIEAMVQLMHLFERNWIIIVLSSDTYGRDNGOLLGERVAR-RDICIAP 240

QY 237 QETLPTLPNQNTSEERQRLIVDKLQOSTARVVVVVSPDLTYHFFNVEVLKQNTFGA 296

Db 241 QEVLPPESSQWRSEQRDLNLDKLRRTSARVVVVVSPDLTYHFFNVEVLKQNTFGF 300

QY 297 VWIASEWAIDPVHLNLTGHLGTLGITITQSPVPIPGFSEFRWGPAGPPLSRTSQS 356

Db 301 VWIASEWAIDPVHLNLTGHLGTLGITITQSPVPIPGFSEFRWGPAGPPLSRTSQS 360

QY 357 YTCNQECNCLNATLSFNITLRLSGERVVYSYSAVAHAHSLGLCDSTCTCKRVVY 416

Db 361 TTCNQDCACLNTYKSFNNILLSGERVVYSYSAVAHAHSLGLCNVRCTKQVY 420

QY 417 PWOLLEETKWNFTLLDHIQIFPDQGVVLAHLEIVQWQDRSQNPFSQSVASYFLQRLK 476

Db 421 PWOLLEETKWNFTLLGRLNLFDDQGDMPMLDIIQWQDLNQNPFSQSVASYFLKRLT 480

QY 477 NIQDSHMTVNTTIPMCMSCRCQSGQKKPVGHVCCFECIDCLPGTFLNHTDEYECQ 536

Db 481 YINNVSWYTPNNTVPVSMCSKSCQPGQMKKSGVLHPCFECIDCLPGTFLNRSADFNL 540

RESULT 14
 ID ADK90718 standard; protein, 843 AA.
 XX
 AC ADK90718;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Mouse taste receptor T1R2 protein.
 XX
 KW gene therapy; taste receptor; T1R3; T1R1; T1R2; taste-induced behavior;
 KW taste topographic map; tongue; taste cell; taste sensory neuron;
 KW brain taste center.
 XX
 OS Mus sp.
 XX
 PN WO2003004992-A2.
 XX
 PD 16-JAN-2003.
 XX
 PF 03-JUL-2002; 2002WO-US021269.
 XX
 PR 03-JUL-2001; 2001US-0302898P.
 PR 10-AUG-2001; 2001US-00927315.
 PR 22-FEB-2002; 2002US-0358925P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Zuker CS, Ryba NJP, Chandrashekar J, Hoon MA, Nelson GA, Zhang Y;
 XX
 DR WPI; 2003-210382/20.
 DR N-PSDB; ADK90721.
 XX
 PT New taste receptors comprising a T1R3 polypeptide and optionally a T1R1
 PT or T1R2 polypeptide, useful as probes for identifying taste cells, and in
 PT gene therapy for correcting acquired and inherited genetic defects.
 XX
 PS Claim 22; SEQ ID NO 8; 119pp; English.
 XX
 CC The invention relates to a novel taste receptor comprising a T1R3
 CC polypeptide and optionally a T1R1 or T1R2 polypeptide. The nucleic acids
 CC and proteins encoding the receptors may be used as probes to identify
 CC taste cells or subsets of taste cells or to dissect taste-induced
 CC behaviors, and in the generation of taste topographic maps that elucidate
 CC the relationship between the taste cells of the tongue and taste sensory
 CC neurons leading to taste centers in the brain. Nucleic acids encoding T1R
 CC protein can be used with highly density oligonucleotide array technology
 CC to identify T1R protein, orthologs, alleles, conservatively modified
 CC variants, and polymorphic variants in this invention. The nucleic acids
 CC may be inserted into vectors for gene therapy correct acquired and
 CC inherited genetic defects and other diseases. Compositions may be
 CC administered to elicit a therapeutic response in the patient. Modulators
 CC of sweet and/or amino acid taste transduction are useful for
 CC pharmacological and genetic modulation of sweet and amino acid taste
 CC ligands, and in food and pharmaceutical industries to customize taste.
 CC This sequence corresponds to the mouse T1R2 protein.
 XX
 SQ Sequence 843 AA;
 Query Match 71.6%; Score 3179; DB 7; Length 843;
 Best Local Similarity 69.1%; Pred. No. 1.8e-294;
 Matches 582; Conservative 114; Mismatches 142; Indels 4; Gaps 2;
 QY 1 MGPRAKTICSLFLLWLVAEP---AENSDFYLPDYLGLGSLHANMKGVHLNPLQVP 57
 DB 1 MGQARTLHLFLLHALPKPVMVGVNSDFHLAGDYLLGGLFTLHANVKSVSHSLQVP 60
 QY 58 MCKEYEVKIVNLMQAMRFAYEEINDDSLPLGVLLGVEIVDVCIYNNVOPVLYFLAH 117
 DB 61 KCNEYMKVIGYLNQAMRFAYEEINNCSSLLPGVLLGYEMDVICYLNNIQGLYFLSQ 120
 QY 118 EDNLLPIQEDSYNISRVRVAVIGPDNSESVMVTFNLSFLPLQITYSAISDELDRKVR 177

Db	121	IDDLEPILKDYQYRPOQVAVIGPDNSESATVSNILSYFLVPQVTSYSAITDKLQDKRRF	180
Qy	178	PALLRTTFSADHVEAMVOLMLHPRNMWILVUSDDYGRDNGOLLGERVARR-DICIAF	236
Db	181	PAMLRTPVSATHTHEAMVQLMVHFQWNI VVLVSDDDYGRNSHLLSRLTNTGDIICIAF	240
Qy	237	QETLPTLQPNQNTSEERQRLVTIVDKLQOSTARVVVVVFPDLTYLHFFNEVLQRNFTGA	296
Db	241	QEVLPVPEPQAVPPEEQDQLNDILKLRRTSARVVVIFSPELSHHFFREVLRNWFTGF	300
Qy	297	VWIASWADIPVLHNLTELGLTFLGTTIQSVIPFGSEFRWGQAGPPPSRISQS	356
Db	301	VWIASWADIPVLHNLTELRLTCTGLGVTIQRVSIQFQFVRHDKPGYRMPNETSLR	360
Qy	357	YTCNQCDNCLNATLSFNTILRSGERVVYSVAVYAHALHSLGCDKSTCTKRVY	416
Db	361	TTNQDCDACNMITESEFNVLMLSGERVVYSVAVYAHALHSLGCDKSTCTKRVY	420
Qy	417	PWOLLEIWKVNFLLDHOIFPDQGDVALHLEIVQWDRSONPQFOSVASYPLQRLK	476
Db	421	PWOLLEIWKVNFLLDHOIFPDQGDVALHLEIVQWDRSONPQFOSVASYPLQRLK	480
Qy	477	NIQDISWHTVNTTIPMSNCSKRCQSGQKKPVGHVCCFECIDCLPGTFLNHTDEVECO	536
Db	481	YISNVSWYTPNNTVPIISMCSKSCQPGQMKKPIGLHPCCFECVCDPDDTYLNRSDENCL	540
Qy	537	ACPNNESYQSETSCFKRQLVFLWHEAPTAVALAALGSLTALIVIFWRHFQPIV	596
Db	541	SCPGSMYSYKNNIACFKRLAFLWHEVPTIVTLLAALGSLTALIVIFWRHFQPIV	600
Qy	597	RSAGPWCFLMLTLLVAVMVVYVGPVKYSTCLCRQALPPLCFTICISCIASVRSQIV	656
Db	601	RSAGPWCFLMLVLLAFAGVYVGPVTVFSCFQAPTVCFVCLSCITVRSQIV	660
Qy	657	CAFKQASRFPRAYSWYVYQGVYSMAFIVLKMVIVVIGMLATGLSPTTDDDPKIT	716
Db	661	CVFKMARRLPSAYGFWMYHGVYVAFITAKVALVAGNMLATTINIGRTDPPDPII	720
Qy	717	IVSCNPNYRNSLLPNTSLDLLLVGVGSFAYMGKELPTNYNEAKFITLSMTFYTSVSL	776
Db	721	ILSCHPNYRNGLLPNTSMDDLVLGVGSFAYMGKELPTNYNEAKFITLSMTFYTSVSL	780
Qy	777	CTFMSAGVGLVATVLDLLVTLNLLAISLGYGPKCYMILFYPERTPAYFNSMIQGYM	836
Db	781	CTFMSVHDGVLVTIMDLLVTLNLLAISLGYGPKCYMILFYPERTPAYFNSMIQGYM	840
Qy	837	RR 838	
Db	841	RK 842	
RESULT 15			
ADM42817			
ID	ADM42817	standard; protein, 843 AA.	
XX	AC	ADM42817;	
XX	DT	03-JUN-2004 (first entry)	
XX	DE	Murine taste receptor protein T1R2 SeqID 61.	
XX	KW	murine; mouse; taste receptor; chemical sensor system; taste; smell;	
XX	KW	artificial sensory organ; olfactory stimulation; food industry;	
XX	KW	hygiene inspection; environmental examination; disease diagnosis;	
XX	OS	Mus musculus.	
XX	PN	WO2003100057-A1.	
XX	PD	04-DEC-2003.	
XX	PD		

Result No.	Query	Score	Match	Length	DB	ID	Description
1	1	4443	100.0	839	2	Q8TE23	Q8te23 homo sapien
2	2	3231	72.7	843	2	Q920R7	Q920r7 rattus norv
3	3	3191	71.8	843	2	Q925I4	Q925i4 mus musculu
4	4	3179	71.6	843	2	Q923J8	Q923j8 mus musculu
5	5	1741	39.2	1465	2	Q7TP27	Q7tp27 rattus norv
6	6	1456.5	32.8	840	2	Q920R8	Q920r8 rattus norv
7	7	1447.5	32.6	842	2	Q925I5	Q925i5 mus musculu
8	8	1446.5	32.6	842	2	Q939G5	Q939g5 mus musculu
9	9	1440.5	32.4	842	2	Q923J9	Q923j9 mus musculu
10	10	1437.5	32.4	842	2	Q939G6	Q939g6 mus musculu
11	11	1351.5	30.4	841	2	Q7RTX1	Q7rtx1 homo sapien
12	12	1289	29.0	929	2	Q8NGZ7	Q8ngz7 homo sapien
13	13	1251	28.2	763	2	Q8TDJ9	Q8tdj9 homo sapien
14	14	1089	24.5	1027	2	Q8JiO4	Q8jiO4 squalus aca
15	15	1079.5	24.3	1078	1	CASR_HUMAN	Q8j180 homo sapien
16	16	1075	24.2	1079	1	CASR_FAT	P48442 rattus norv
17	17	1075	24.2	1085	1	CASR_BOVIN	P35384 bos taurus
18	18	1071	24.1	1079	1	CASR_MOUSE	Q97g96 mus musculu
19	19	1071	24.1	1079	2	Q80ZJ8	Q80Za8 rattus norv
20	20	1057	23.8	940	2	Q736J5	Q736j5
21	21	1051	23.7	941	2	Q6XAF1	Q736j5 fugu rubrip
22	22	1051	23.7	941	2	AAP79925	Q6xaf1 salmo salar
23	23	1045.5	23.5	858	2	Q923K1	Aap79925 salmo sal
24	24	1044	23.5	941	2	Q6XAF3	Q923k1 rattus norv
25	25	1044	23.5	941	2	AAP79923	Q6xaf3 salmo salar
26	26	1038.5	23.4	928	2	Q70VB1	Aap79923 salmo sal
27	27	1038.5	23.4	928	2	CAD59483	Q70vb1 rattus norv
28	28	1033.5	23.3	928	2	Q8K4Z6	Cad59483 rattus no
29	29	1029.5	23.2	858	2	Q925D8	Q8k4z6 mus musculu
30	30	1026.5	23.1	858	2	Q923K0	Q925d8 mus musculu
31	31	1025.5	23.1	858	2	Q925A4	Q923k0 mus musculu

QY 121 LLPIQEDYNYISRVAVVGPDSSEVMTVANFLSLFLLPQITYSALSDELKRVFPAL 180
 DB 121 LLPIQEDYNYISRVAVVGPDSSEVMTVANFLSLFLLPQITYSALSDELKRVFPAL 180
 QY 181 LRTPPSADHVEAMVQLMLHFRWNWIIIVLSSDYGRDNGQLGGERVARRDICIAPQETL 240
 DB 181 LRTPPSADHVEAMVQLMLHFRWNWIIIVLSSDYGRDNGQLGGERVARRDICIAPQETL 240
 QY 241 PTLQPNQNTSEERQRLVTIVDLQOSTARVVVVFSPDLTYHFFNEVLKQNTGAVWIA 300
 DB 241 PTLQPNQNTSEERQRLVTIVDLQOSTARVVVVFSPDLTYHFFNEVLKQNTGAVWIA 300
 QY 301 SESWAIDPVNLHNTLHGLTGLTIGITQSVPIGFSEFREFWGPAGPPPLSRSTSQTEN 360
 DB 301 SESWAIDPVNLHNTLHGLTGLTIGITQSVPIGFSEFREFWGPAGPPPLSRSTSQTEN 360
 QY 361 QECDCNCLNATLSFNTILRLSGERVVSVYSAVAVAHALSHLLGCDKSTCTKRVVYPWL 420
 DB 361 QECDCNCLNATLSFNTILRLSGERVVSVYSAVAVAHALSHLLGCDKSTCTKRVVYPWL 420
 QY 421 LEEIKVNFLLDHOIFPDQGVVALHLEIVQWDRSQNPFSQSVASYYPQLQKNIQD 480
 DB 421 LEEIKVNFLLDHOIFPDQGVVALHLEIVQWDRSQNPFSQSVASYYPQLQKNIQD 480
 QY 481 ISWHTVNTTIPMSMCKRCSGQKPKVGVHVCCEICDCLPGTFLNHTDEYECQACPN 540
 DB 481 ISWHTVNTTIPMSMCKRCSGQKPKVGVHVCCEICDCLPGTFLNHTDEYECQACPN 540
 QY 541 NEWSQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFTQPIVRSAG 600
 DB 541 NEWSQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFTQPIVRSAG 600
 QY 601 GPMCFMLTLVAVVMPVVPVGPVKSTCLCROALFPLCTICICIAVRSFOIVCAFK 660
 DB 601 GPMCFMLTLVAVVMPVVPVGPVKSTCLCROALFPLCTICICIAVRSFOIVCAFK 660
 QY 661 MASRFRAYSVWRYVQGPVYSMAFITVLMVIVIGMLATGLSTPTTRDPPDKITVSC 720
 DB 661 MASRFRAYSVWRYVQGPVYSMAFITVLMVIVIGMLATGLSTPTTRDPPDKITVSC 720
 QY 721 NPYNRSLLFNTSLDLSLVVGFSPAYMKGELPTNYNEAKFITLSMTPTFTSSVSLCTFM 780
 DB 721 NPYNRSLLFNTSLDLSLVVGFSPAYMKGELPTNYNEAKFITLSMTPTFTSSVSLCTFM 780
 QY 781 SAYSGVLVTIVDLVTVNLNLAISLGYGPKCYMILFYPERNTPAYFNSMIQGYTM 839
 DB 781 SAYSGVLVTIVDLVTVNLNLAISLGYGPKCYMILFYPERNTPAYFNSMIQGYTM 839

RESULT 2

Q920R7 PRELIMINARY; PRT; 843 AA.
 AC Q920R7;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE Putative taste receptor TR2 (fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar;
 RA Hoon M.A., Adler E., Lindemeier J., Battey J.F., Ryba N.J.,
 RA Zuker C.S.;
 RT "putative mammalian taste receptors: a class of taste-specific GPCRs
 with distinct topographic selectivity";
 RL Cell 96:541-551 (1999).
 DR EMBL; AF127390; AAD18070.1; --
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. .; IEA.

DR GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR001828; ANF receptor.
 DR InterPro; IPR000337; GPCR Mgr.
 DR InterPro; IPR011500; NCD3G_GPCR.
 DR Pfam; PF00003; 7tm_3; 2.
 DR Pfam; PF01094; ANF receptor; 1.
 DR Pfam; PF07562; NCD3G; 1.
 DR PRINTS; PR00248; GPCRMR.
 DR PROSITE; PS02559; G_PROTEIN_RECEP_F3_4; 1.
 KW Receptor.
 FT NON_TER 843 843
 SQ SEQUENCE 843 AA; 95799 MM; D23AC22D21E04988 CRC64;

Query Match 72.7%; Score 3231; DB 2; Length 843;
 Best Local Similarity 70.8%; Pred. No. 3.3e-231;
 Matches 596; Conservative 109; Mismatches 133; Indels 4; Gaps 2;

QY 1 MGPRAKTIICSLFLLVLAEP---AENSDFYLPDGLGGLFSLHNMKGIVHNFLOVP 57
 DB 1 MGPQARTCLLSLLHVLKPKGLVENSDFHLAGDVLGLLFTLHANVKISHLUSYLQVP 60
 QY 58 MCKEYEVKVIYNLMQAMFAVEEINNDSLLPGVLGYEIVDVYCISSNNVQPVLYFLAH 117
 DB 61 KCNEFTMKVLYGNLMQAMFAVEEINNCSLLPGVLGYEIVDVYCISSNNHPLGLYFLAQ 120
 QY 118 EDNLLPTQEDYSNYISRVAVVGPDSSEVMTVANFLSLFLLPQITYSALSDELKRVF 177
 DB 121 DDLLPILKDYQVMPHVAVVGPDSSEVMTVANFLSLFLLPQITYSALSDELKRVF 180
 QY 178 PALRTTPSADHVEAMVQLMLHFRWNWIIIVLSSDYGRDNGQLGGERVARRDICIAP 236
 DB 181 PSMRLTTPSADHVEAMVQLMLHFRWNWIIIVLSSDYGRDNGQLGGERVARRDICIAP 240
 QY 237 QETLPTQPNQNTSEERQRLVTIVDLQOSTARVVVVFSPDLTYHFFNEVLKQNTG 296
 DB 241 QEVLPPESSQVWRSEORQDLNLDKLRTSARVVVVFSPDLTYHFFNEVLKQNTG 300
 QY 297 VWIASEWAIDPVNLHNTLHGLTGLTIGITQSVPIGFSEFREFWGPAGPPPLSRSTS 356
 DB 301 VWIASEWAIDPVNLHNTLHGLTGLTIGITQSVPIGFSEFREFWGPAGPPPLSRSTS 360
 QY 357 YTCNQECDCNCLNATLSFNTILRLSGERVVSVYSAVAVAHALSHLLGCDKSTCTKRV 416
 DB 361 TTCNQDCDACLNTTFSNNILISLGERVVSVYSAVAVAHALSHLLGCDKSTCTKRV 420
 QY 417 PWQLLEIKVNFLLDHOIFPDQGVVALHLEIVQWDRSQNPFSQSVASYYPQLQK 476
 DB 421 PWQLLEIKVNFLLDHOIFPDQGVVALHLEIVQWDRSQNPFSQSVASYYPQLQK 480
 QY 477 NIQDISWHTVNTTIPMSMCKRCSGQKPKVGVHVCCEICDCLPGTFLNHTDEYECQ 536
 DB 481 YINNVSWYTPNNTVPSMCKRCSGQKPKVGVHVCCEICDCLPGTFLNHTDEYECQ 540
 QY 537 ACPNNEVSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFTQPI 596
 DB 541 SCPGSMWSYKNDITCFQRRTFLWHEVPTIIVALLAALGFLSTLAILVIFWRHFTQPI 600
 QY 597 RSAGGPMCFMLTLVAVVMPVVPVGPVKSTCLCROALFPLCTICICIAVRSFOIV 656
 DB 601 RSAGGPMCFMLTLVAVVMPVVPVGPVKSTCLCROALFPLCTICICIAVRSFOIV 660
 QY 657 CAFKMASRFRAYSVWRYVQGPVYSMAFITVLMVIVIGMLATGLSTPTTRDPPDKIT 716
 DB 661 CVFKMARLPSAYSFWRYVQGPVYSMAFITVLMVIVIGMLATGLSTPTTRDPPDKIT 720
 QY 717 IVSCNPNYRNSLLFNTSLDLSLVVGFSPAYMKGELPTNYNEAKFITLSMTPTFTSSV 776
 DB 721 ILSCHPNYRNSLLFNTSLDLSLVVGFSPAYMKGELPTNYNEAKFITLSMTPTFTSSV 780
 QY 777 CTFMSAYSGVLVTIVDLVTVNLNLAISLGYGPKCYMILFYPERNTPAYFNSMIQGY 836
 DB 781 CTFMSAYSGVLVTIVDLVTVNLNLAISLGYGPKCYMILFYPERNTPAYFNSMIQGY 840


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QY 837 RR 838
Db 841 RK 842

RESULT 3
Q92514 PRELIMINARY; PRT; 843 AA.
AC Q92514;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Candidate taste receptor T1R2.
GN Name=Tas1r2; Synonyms=T1r2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21219400; PubMed=11119557;
RA Montmayeur J.P., Liberles S.D., Matsunami H., Buck L.B.;
RT "A candidate taste receptor gene near a sweet taste locus.";
RL Nat. Neurosci. 4:492-498(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Montmayeur J.-P., Liberles S.D., Matsunami H., Buck L.B.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF337041; AAK39438.1; -.
DR MGD; MGI:193546; Tas1r2.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm 3; 2.
DR Pfam; PF01094; ANF receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00248; GPCRMR.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 843 AA; 95735 MW; 0543834EA7AC2E CRC64;

Query Match
Best Local Similarity 69.4%; Score 3191; DB 2; Length 843;
Matches 584; Conservative 113; Mismatches 141; Indels 4; Gaps 2;

QY 1 MGPRAKTICSLFLLWVLAEP---AENSDFYLPDGYLLGLGFLSHANMKGIHVLNFIQVP 57
Db 1 MGPRARTLHLFLLLHALPKPVMVLYGNSDFHLGADYLLGLGFLSHANVKSVSHLYLQVP 60
QY 58 MCKEVEVKGIVNLMQMRFAVEEINNSDLPGLVGLVEIVDVCYISNNVQPVLYFLAH 117
Db 61 KCNEYNMKVLGYNLQMAREFAVEEINNCSSLLPGVLLGYEMVDVCLSNIIQGLYFLSQ 120
QY 118 EDNLLPIQEDSNYSIRVVAVIGPDSNVMVAVNLSFLIPQITYSAISDELKDKVRF 177
Db 121 IDDFLPIKDSQYRPQVAVIGPDSNVAITVSNILSYFLPQVITYSAITDKLDRKRF 180
QY 178 PALLRTTFSADHHVAMVQLMLHFRWNWILVLSDDTYGRNQGLLGERVARR-DICIAF 236
Db 181 PAMLRVTSATHIEAMVQLMVHFMVQNNVILVLSDDTYGRNSHLLSRLTNWTDICIAF 240
QY 237 QETLTPQNMNTSEERQRLVTVIIVDKLQQSTARVVVFPSPDLTYLHFNEVLRQNTFGA 296
Db 241 QEVLPVPFNQAVRPEEQDQLNLDKLRRTSARVVVIFSPSLSHNFFREVLRNWTFG 300
QY 297 VWIASWAIDPVHLNLTGHLGTLGTLTQSVIPGFSFRFPGVAGPPPLSRTSQS 356
Db 301 VWIASWAIDPVHLNLTGHLGTLGTLTQSVIPGFSFRFVRHDKPEYMPMPNETSLR 360

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RESULT 4

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Q923J8 PRELIMINARY; PRT; 843 AA.
AC Q923J8;
ID Q923J8;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Sweet taste receptor T1R2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC MEDLINE=21400448; PubMed=11509186;
RA Nelson G., Hoon M.A., Chandrasekar J., Zhang Y., Ryba N.J.P.,
RA Zuker C.S.;
RT "Mammalian sweet taste receptors.";
RL Cell 106:381-390(2001).
DR EMBL; AY032623; AAK51604.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm 3; 2.
DR Pfam; PF01094; ANF receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PF00248; GPCRMR.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 843 AA; 95752 MW; FD3C6B9B23270DA3 CRC64;

Query Match
71.6%; Score 3179; DB 2; Length 843;

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Best Local Similarity 69.1%; Pred. No. 2.4e-227;
Matches 582; Conservative 114; Mismatches 142; Indels 4; Gaps 2;

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QY      1  MGPRAKTICSLFELLWLAEP---AENSDFVLPGDYLLGGLFSLHANMKGVHLNFIQVP 57
Db      1  MGQPARLTHLLFLLHALPKPVMVLGNSDFHLADYLLGGLFTLHANVKSVSHLSYIQVP 60

QY     58  MCKEYEVKVIQYNLMQAMRFAVEEINNDSLLPGVLLGYEIVDYCYISNNVQPVLYFLAH 117
Db     61  KCNEYNMKVLGYNLMQAMRFAVEEINNCSLLPGVLLGYEMVDVCYLSNNIQPLGYFLSQ 120

QY    118  EDNLLPIQEDYSNIYISRVAVIGDNGSESVMVTANFLSLFLLPQITYSATISDELKDKRF 177
Db    121  IDDFLPILKDYQYRPOVAVIGPDNGSESATVSNILSYFLVPQVITYSAITDKLQDKRRF 180

QY    178  PALLRTTPSADHVEAMVQMLHFRMNIIVLVSSDTYGRDNGQLLGERVARR-DICIAF 236
Db    181  PAMLRTPSATHIEAMVQLMHVHPQMWIIVLVSDDDYGRNSHLLSGRLTNTGIDICIAF 240

QY    237  QETLPTIQNNQNTSEERQRLVITVDKLOQSTARVVVVFSPDLTYLHYFNFVLRQNFQA 296
Db    241  QEVLVPEPQAVRPEQDQLNDILKLRRTSARVVVIFSDLSLHNPFREVLWRMNFQF 300

QY    297  VTIASSWAIDPVLHNLTELGHTGTFIGITIQSVPIPGFSFRFWRGPOAGPPPLSRTSQS 356
Db    301  VTIASSWAIDPVLHNLTELHRTGTFLGVTIQVSIQFSQFRVHRHDPGXYRMPNETSLR 360

QY    357  YTCNOECDNCLNATLSNFTILRSGERVVYSVAVAVAHLSLGLCDKSTCKRVVY 416
Db    361  TTCNQDCDCAWNITFESFNNVLMLSGERVVYSVAVAVAHTLHRLLHCNQVCTKIQVY 420

QY    417  PWOLLEIKVNFYLLDHDQIFPDQGDVALHLEIVQWMDRSQNPQFQSVASYPLQORQK 476
Db    421  PWOLLRREIHWNFYLLGNLQFDEQGDPMMLDIIQWQGLSQNPFQSIASVSPETRLT 480

QY    477  NIQDISWHTVANTIPMSCKSRKQSGQKKKPVGIHVCCEICIDCLPGTFLHTEDEYBQ 536
Db    481  YISNVSWYTPNNTVPIISMCKSKSCOPQWKKPQIGLHPCCFECVDCPDTYLNRSVDFNCL 540

QY    537  ACPNNEWSQSETSCFKQLVPLEHHEAPTIAVALLAALGFLSTLAILVPMRHFOQTPV 596
Db    541  SCPGSMYSKYNIACFKRLAPLEWHVEPTIVITLALGFLSTLAILLIFWRHFQTPW 600

QY    597  RSAGGPMCFMLTLLVAYMVVYVVGPKVSTCLCQALFPLCFTICISIAVRSFQIV 656
Db    601  RSAGGPMCFMLVPLLLAFGMPVYVVGPPVFCFCRQAFVTVCFSVCLSCITVRSFQIV 660

QY    657  CAFKQAGSFPRAYSYYWYQGPYSMAFITVLKQVIVIGMLATGLSPTRTRDDPKIT 716
Db    661  CVFKMARLPSAYGEMWYHGYPVFAFITA VKVALVAGNMLATTINPIGRITDPPDENT 720

QY    717  IVSCNPNYRNSLLFNTSLDLLSVVGFSAFMGKELPTNYNEAKFTLSMTFYFTSSVSL 776
Db    721  ILSCHPNYRNGLLFNTSMDLLSVLGFSAFMGKELPTNYNEAKFTLSMTFYFTSSISL 780

QY    777  CTFMSYGVGLVTIVDLIVTLNLLAISLGYPGPKCYMLFPERNTPAYFNSMIQGYTM 836
Db    781  CTFMSVHGDGLVTIMDLLVTLNFLAIGLYGFGPKCYMLFPERNTPAYFNSMIQGYTM 840

QY    837  RR 838
Db    841  RK 842

RESULT 5
Q7TP27
ID Q7TP27 PRELIMINARY; PRT; 1465 AA.
AC Q7TP27;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
OS Bal-651.
DE Rattus norvegicus (Rat).

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Q920R8;
 01-MAY-1999 (TrEMBLrel. 10, Created)
 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative taste receptor TR1 (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar;
 RX MEDLINE=99159821; PubMed=10052456;
 RA Hoon M.A., Adler E., Lindemeier J., Battey J.F., Ryba N.J.,
 RA Zuker C.S.;
 RT "Putative mammalian taste receptors: a class of taste-specific GPCRs
 with distinct topographic selectivity."
 RL Cell 96:541-551 (1999).
 DR EMBL; AF127389; AAD18069.1; .
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR001828; ANF_receptor.
 DR InterPro; IPR000345; GPCR_Mgr.
 DR InterPro; IPR011500; NCD3G_GPCR.
 DR Pfam; PF000003; 7tm_3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR Pfam; PF07562; NCD3G; 1.
 DR PRINTS; PR00248; GPCRMR.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR PROSITE; PS0259; G_PROTEIN_RECP_F3_4; 1.
 KW Receptor.
 FT NON_TER
 FT TER
 SQ SEQUENCE 840 AA; 93496 MW; 1FCFB7EFC6B45DB CRC64;
 Query Match 32.8%; Score 1456.5; DB 2; Length 840;
 Best Local Similarity 39.7%; Pred. No. 2.8e-99;
 Matches 327; Conservative 123; Mismatches 344; Indels 29; Gaps 12;
 27 FVLPGDYLLGLGFLSHANKGVHINFLQVPMK-KEYEVKVTGYNNMQMRFAVBEINND 85
 31 FSLPGDFLLAGFLSHGDCLOVRHRL--VTSRDRPDSFNGHYHLFOAMRTVEEINNS 88
 86 SSLPGVLLGVEIVDVYCSNNVQVLYFLAHE-DNLLPIQEDYSNYLSRVAVVIGPDS 144
 89 SALLFNITGLYELDVCSANVATLRVLAQGPRIEIQDLNRHSKVVAFIGPONT 148
 145 ESMVTVANFLSLFLPQITYSAISDELDRKVRFPALLRTTPSADHHVAMVOLMLHFRWN 204
 149 DHAVTTAALLGFLMPLVSYEASSVVLGAKRFPSPFLRTVPDRHQVEVMVQLQSGWV 208
 205 WILVLVSDTYGRDNGQLGERVARDICIAFOETLPTLPQNQNTSEERQLVTIVDKL 264
 209 WISLIGSYGDYGLGVQALEELAVPRGICVAFKDIVPF-----SARVGDPRMQSMQHL 262
 265 QOSTARVVVVVSPDLTLVHFFNEVLKQNTGAVWIASESWAIDPVLHNLTLGLHGTGLG 324
 263 AQARTVVVVVSNRLHARVFRSVVLANTGKVVVASEDAWISTVITSGQGGTGLVIG 322
 325 ITIQSVPIGFSEFEPWGPAGPPPLSRISQSYTC--NQECDNCLNATLSFNLTILRSGE 382
 323 VAVQORQVGLKEFEESVYRAVTAAPSACPEGSWCSTNQLCRECHTFTTRNPTLGFSM 382
 383 RVVSYVYSAVAVAHLSLGLCDKSTCKRVVYVWQLLEELKWNFNLLDHIQIFPDQ 442
 383 SAAYRVYEAIVAVAHGLHQLGCTSEICSRGVPYVWQLLQYIKVFNFLHENTVAFDDNG 442
 443 DVALHLEIVQWOWDRSONPFSQV--ASYVPELQRLKNIQDISWHTVNTIIPMSCKKQC 500
 443 DTLGYDIIADWNGPWTFFELIGSASLSPVHLDI-NKTKIQWGHKNQVPSVCTTDC 501
 501 SQKKKPVGIHVCCPECIDCLPGTFLNHTDEYEQACPNNEWSQSETSCFKRQLVLE 560

Db 502 AGHRRVWVGHSCCECPVCEAGTFLNMSE-LHIQPCQTEWAPKSTCTCPRTVEFLA 560
 QY 561 WHEAPTIALLAALGFLSTLAILV-----IFWRHFQPIVRSAGGPMCFMLTLALLVA 614
 Db 561 WHE--PISLVLIAA-----NTLLLLLVGTAGLFAWHFHTPVVRSAGGRLCFMLGSLVAG 614
 QY 615 YMVVPVYVGPVKVSTCLCRQALFPLCFCTICISCIARSFOIVCAFKWASRFPAYSVYWR 674
 Db 615 SCSFYSFFGEPTVPACLRQPLFSGLAFLSCLTIRSFQLVIIIFKSTKVPFTFYRTWAQ 674
 QY 675 YQGPYVSMAFITVLKRWIVVIGMLATGLSPTRTDDPKITIVSCNPNYRNLSLFTNSL 734
 Db 675 NHGAGLFVIVSVTVHLLICLTWLVMMVTRP-TREYQRFPHLVILCTEVSNGVGLLAPTH 733
 QY 735 DLLLSVGVGFSFAYMGKELPTNNNEAKFTLSMTFTVTSVLSCTFMSYSGVLVITVDLL 794
 Db 734 NILLSISTFVCSYLGKELPENYNEAKCVTFSLNLFVSWIAFFTMASTIYQGSYLPVNV 793
 QY 795 VTVMLNLAISLGYGFGKCYMILFYERNTPAVFNSMIQGYTMR 837
 Db 794 AGLTTLGGFGFYFLPKCYVILCRPELANTEHFQASIODYTRR 836
 RESULT 7
 Q925I5 PRELIMINARY; PRT; 842 AA.
 AC Q925I5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Candidate taste receptor TIR1.
 GN Name=Tas1r1; Synonyms=Tir1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=21219400; PubMed=11319557;
 RA Montmayeur J.-P., Liberles S.D., Matsunami H., Buck L.B.;
 RT "A candidate taste receptor gene near a sweet taste locus."
 RL Nat. Neurosci. 4:492-498 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF317040; AAK39437.1; .
 DR HSP; P23385; LEWK.
 DR MGI; MGI:1927505; Tas1r1.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR001828; ANF_receptor.
 DR InterPro; IPR000068; Ca_sens_receptor.
 DR InterPro; IPR000345; GPCR_Mgr.
 DR InterPro; IPR011500; NCD3G_GPCR.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR Pfam; PF07562; NCD3G; 1.
 DR PRINTS; PR00592; CASENSINGR.
 DR PROSITE; PR00248; GPCRMR.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR PROSITE; PS0259; G_PROTEIN_RECP_F3_4; 1.
 KW Receptor.
 SQ SEQUENCE 842 AA; 93471 MW; FDBA0CC1BD45DEE7 CRC64;
 Query Match 32.6%; Score 1447.5; DB 2; Length 842;
 Best Local Similarity 40.0%; Pred. No. 1.3e-98;
 Matches 330; Conservative 121; Mismatches 340; Indels 35; Gaps 15;

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RC STRAIN=129P3/J;
RX MEDLINE=21030739; PubMed=11178737;
RA Li X., Inoue M., Reed D.R., Huque T., Puchalski R.B., Tordoff M.G.,
RA Ninomiya Y., Beauchamp G.K., Bachmanov A.A.;
RT "high-resolution genetic mapping of the saccharin preference locus
RT (Sac) and the putative sweet taste receptor (T1R1) gene (Gpr70) to
RT mouse distal Chromosome 4.";
RL Mamm. Genome 12:13-16(2001).
DR EMBL; AF301162; AAK07092.1; -.
DR HSP; P23385; IEWK.
DR MGD; MGI:1927505; Tas1r1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF receptor.
DR InterPro; IPR000068; Ca sens. receptor.
DR InterPro; IPR000345; CyC heme_BS.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00592; CASENSINGR.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
FT NON_TER.
FT SEQUENCE.
QY 27 FYLPDGYLLGGLSLHANMKGIHLNLFQVPMC--KEYEVKIVGYNLMQAMRFVAVEEINND 85
Db 33 FSLPGDFLLAGLSLHADCLQVRHPL--VTSCDRSDFNGHGLFQAMRFTVEEINNS 90
QY 86 SSLPGVLLGYEIVDVCYISNNQVLYFLAHE--DNLLPIQEDYSNYSRVVAVIGPDS 144
Db 91 TALLPNITLGYELVDVCSSNNVATLRVLAQQTGHLQMDLRNHSKVVALLIGPNT 150
QY 145 ESMVTVANFSLFLLPOITYSASDELKRVFPALLRTTPSADHHVEMVQLMHLFRN 204
Db 151 DHAVTTAALLSPFLMPLVSEASVILSGRKFESFLRTIPSDKYQVEIVRLQSGFGV 210
QY 205 WIIVLVSDTYGRDNGQLGGERVARRDICIATQETLPTLQPNQNTSEEROLVTIVDKL 264
Db 211 WISLVGSDYGVQGVQALELAPRGICVAFKDVPL---SAQAGDPRMQRML--RL 264
QY 265 QQSTARVVVVFSPDLTYLHFFNEVLRQNTGAVMIASEWAIDPVLHNLTELHGLGTLFG 324
Db 265 ARARTVVVVFSENRHLGAGVFRSVVLANLTGKWIASEDWAISTVITNPGIQTGTVLG 324
QY 325 ITIQSVPIPGSEFRWGPOA--GPPPLSRTSQSYTCNOECDNCLNATLSNTILRLSGE 382
Db 325 VAIQORQVPLGKFEESYVQAVTGAPRTCPGSGWCGTNQLCRECHAFTHMPELGAFSM 384
QY 383 RVVYSVYSAVVAHAHLHLGCDKSTCTKRVVYPWOLLEBIKWNFTLLDHLQIFPDQ 442
Db 385 SAANNVYEAIVAHGLHQLLGTSCTGARGVTPWQLLQYIKVFNLLHKKTVAFDNG 444
QY 443 DVALHLEIVQWDRSQNPFSV--ASYPLQRLQKNIQDISWHTVNNTPIMSCSKRCQ 500
Db 445 DPLGYDIIADWNGPEWTFEIVGSASLSPVHLDI--NKTIKQHGKKNQVPSVCTRDL 503
QY 501 SQGKKKPVGIHVCCPECIDCLPGFLNTEDEYEQACPNNNSVQSETSCKEQLVLE 560
Db 504 EGHRLVMSGHCCFECMPCBAGTFLN--TSELHTCQPCGTBEWAPEGSSACFSRTVEFLG 562
QY 561 WHEAPTTAVALLAALGFLSLTALIVIF-----WRHFQTPIVRSAGGPMCFMLTLIV 613
Db 563 WHE--PISLVLLA-----NTLLLLLLICTAGLFAWR--LHTPVRSGAGRLCFMLGSLVA 615
QY 614 AMVVPVYVGPVKVSTLCRALPCLCTICISCIASVRSFOIVCAFKMASRPPRAYSVW 673
Db 616 GCSLSYSPFGKPTVPACLLRQLPSLGAIFLSCLTIRSFQVLIIFKFTKVPFYHTWA 675
QY 674 RYQGYVSMATITVLKMY--IWIIGLATGLSPTRTPDPPDKITIVSCNPNYRNSLLFN 731
Db 676 QNHGAGI---FVIVSSTVHLELCITLWLTWTPRTREYQRPFLHVLLECTEVSNGFLVA 732
QY 732 TSLDLLLSVGVGFSAYMGKELPTVYNEAKFTLSMTFTYFTSSVLSICTFMSAYSGVLTV 791
Db 733 FAHNILLSISTFVCSYLGKELPENYNEAKCVTFSLHLHFVSWIAFFTMSSYIQSYLPAV 792
QY 792 DLLVTVNLALISLGYGPKCYMILFYPERNTPAYFNSMIQYTMR 837
Db 793 NVLAGLATLSGFGSYFLPKCYVILCRPELNNTHEFOASIQDYTR 838

RESULT 8
Q99PG5 PRELIMINARY; PRT; 842 AA.
AC Q99PG5;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Putative sweet taste receptor T1R1 (Fragment).
GN Name=Tas1r1; Synonyms=Gpr70;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR001828; ANF_receptor.
 DR InterPro; IPR000068; Ca_sens_receptor.
 DR InterPro; IPR000345; CytC_heme_Bs.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR InterPro; IPR011500; NCD3G_GPCR.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR Pfam; PF01562; NCD3G; 1.
 DR PRINTS; PR00592; CASENSINGR.
 DR PRINTS; PR00248; GPCRMR.
 DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
 DR PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.
 KW Receptor.
 FT NON_TER 842 842
 SQ SEQUENCE 842 AA; 93425 MW; 58826C43F5DD352E CRC64;
 Query Match 32.4%; Score 1437.5; DB 2; Length 842;
 Best Local Similarity 39.8%; Pred. No. 7.3e-98;
 Matches 329; Conservative 122; Mismatches 340; Indels 35; Gaps 15;
 QY 27 FYLPDGYLLGGLFSLHANMKGI VHLNLFQVPMC-KEYEVKIVGYNLMQAMRFAVEEINND 85
 Db 33 FSLPGDFLLAGLSHADCLQVRHPL--VTSCDRSDSFNGHGYHLFQAMRFTVEEINNS 90
 QY 86 SSILPGVLGYEIVDVCYISNNQPVLYFLAHE--DNLLPIOEYDSYISRVAVIGPDNS 144
 Db 91 TALLPNTLLGYELDYSESNNYATLURVLAQQTGHLQWDRDNRHSSKVVALIGDNT 150
 QY 145 ESWMTVANFLSLFLLPQITYSALSDLRKVRFPALLRTTPSDADHVEAMVQMLMHPRN 204
 Db 151 DHAVTTAALLSPFLMPLVSVEASSVLSKRPFLRTTPSKYQVEVIVRLQLSGFW 210
 QY 205 WIIVLSSDYGRDNQGLGERVARRDICTAFQETLPTLPQNMNTSEERQLVTVVDKL 264
 Db 211 WISLVSGYDYGQLGVQALEELATPRGICVAFKNVPL---SAQAGPRMQRMML---RL 264
 QY 265 QOSTARVVVFPDLYLHYFENEVLRFNFTGAWIASESWAIDPVLHNLTELGHGLFLG 324
 Db 265 ARATTVVVFNHLDGVFRSVVLANLTKGWIASESWAIDPVLHNLTELGHGLFLG 324
 QY 325 ITIQSVPIPGFSEPREMGPOA--GPPPLSRTSQSYTCNQECNCLNATLSFNITLRLSGE 382
 Db 325 VALQORQVPLGKEFEESVQAVMGAPRTCPBGSWCGTNQLCRECHFTTNMPELGAFSM 384
 QY 383 RVVSVYSVAVVAHALSHLGLCDKSTCTKRVVVPWQLLEIKVKNVTLLDHQIFPDQG 442
 Db 385 SAAYNVYEA VAVAHGLHQLIGCTSGTCARGVHPWQLLOQIYKVNFLHKKTVAFDDKG 444
 QY 443 DVALHLRIWOWDRSONPQSV--ASYPLQRLQKNIQIDISHTVANNITPMSCKRCQ 500
 Db 445 DPLGYDIIADWNGPWTTEVIGSASLSPLVLDI--NKTQIOMGKNQNPVSVCTRDCL 503
 QY 501 SGQKKFVGHVCCFECIDCLPGFLNHTEDYECCACPNNEWSQYSETSCFRQLVPLE 560
 Db 504 EGHRLVMGSHCCFECMPCBAGFLN--TSELHTCQPCGTEWAEWAGSSACFSRTVEFLG 562
 QY 561 WHEAPTTAVALLAALGLSTLAILVIP-----WRHFTPIVTSAGSPCMFLMTLLLV 613
 Db 563 WHE--PISLVLLAA---NTLLLLIGTAGLFAWR--LHTPVVRSAGRLCFLMLGLSLVA 615
 QY 614 AYVVPVVGPKYSTLCROALPCLCTICISGIAVRSPOIVCAFKMASRFPRAYSVWV 673
 Db 616 GSCSLYEFKPTVPACLLRQPLFSLGFAIFLSCLTIRSFOLVIRFESTKVPFTYTW 675
 QY 674 RYQGPVSMAFITVLKMW--TWIGMLATGLSPTRTDPDPKXITIVSCNPYNSLLFN 731
 Db 676 QNHGAGI--FVIVSSVTHLFLCLTTLAMWTPTREYQRPPLHVLILECTEVSNGFLVA 732
 QY 732 TSLDLLLSVGVGSFAYMGKELPTWYNEAKFTLSNTFFYTSVSLCTFMSAYSGLVITIV 791

Db 733 FAHNILLSISTFVCSYLGKELPENYNAKCVTSLLLHFWSWIAFTFTMSIYQGSYLPVAV 792
 QY 792 DILVTVTNLNLALISGLGYGPKCYMILFYPERNTPAYFNSMIQGYTMR 837
 Db 793 NVLAGLATLSGSGFYLPKCVILCPELNTEHFQASIQDYTRR 838
 RESULT 11
 QYRTX1 PRELIMINARY; PRT; 841 AA.
 ID QYRTX1
 AC QYRTX1
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Taste receptor.
 GN Name-TAS1R1;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21927605; PubMed-11917125;
 RA Li X., Staszewski L., Xu H., Durick K., Zoller M., Adler E.;
 RT "Human receptors for sweet and umami taste."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4692-4696(2002).
 CC -I- MISCELLANEOUS: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
 DR EMBL; BK000153; DAA00012.1;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. .; IEA.
 DR InterPro; IPR001828; ANF_receptor.
 DR InterPro; IPR000068; Ca_sens_receptor.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR InterPro; IPR011500; NCD3G_GPCR.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR Pfam; PF01562; NCD3G; 1.
 DR PRINTS; PR00592; CASENSINGR.
 DR PRINTS; PR00248; GPCRMR.
 DR PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.
 KW Receptor.
 SQ SEQUENCE 841 AA; 93073 MW; E80072B267D0216 CRC64;
 Query Match 30.4%; Score 1351.5; DB 2; Length 841;
 Best Local Similarity 37.5%; Pred. No. 1.8e-91;
 Matches 315; Conservative 131; Mismatches 354; Indels 41; Gaps 17;
 QY 16 WTLA-BPAENS-DPYLPDGYLLGGLFSLHANMKGI VHLNLFQVPMC-KEYEVKIVGYNLM 72
 Db 19 WAFACHSTESSPDFTLPDGYLLAGLPLHSGCLQVRHPL--EVTLCDRSCSFNEHGYHLF 76
 QY 73 QAMRFAVEEINNDSSLLPGVLGYEIVDVCYISNNQPVLYFLA---HEDNLLPIOEYD 128
 Db 77 QAMRLGVEEINNDSSLLPGVLGYEIVDVCYISNNQPVLYFLA---HEDNLLPIOEYD 133
 QY 129 SNVISRVAVVIGPDNSSEVMTVANFLSLFLLPQITYSALSDLRKVRFPALLRTTSPAD 188
 Db 134 LHSVPTVAVIGPDNSTNRAATTAALLSPFLVPMISYASSETLSVKRQYFSFLRTIENDK 193
 QY 189 HHVEAMVQMLMHPRNMIIVLVSDDTYGRDNQGLGERVARRDICTAFQETLPTLPQNM 247
 Db 194 YQVETVLLQLKQFWTWISLVGSDDDYGLGVQALENQATCGGICIAFKIMPFSQAVGD 253
 QY 248 NMTSEERQLVTVVDKLQOSTARVVVFPDLYLHYFENEVLRFNFTGAWIASESWAID 307
 Db 254 -----ERQCLMRHLAQAGATVVVVFSSRQLARVEFESVLTNLTGKWWIASEAWLS 306
 QY 308 PVLHNLTELGHGLFTGLITIQSVPIPGFSEPREMGPOA---GPPPLSRTSQSYTCNQEC 364
 Db 307 RHITGVPGIQRIGWLVGVAIQKRAVPGIKAFEEAYARADKKAPRCHKGSWC--SSNQLCR 365

QY 365 NCLNATLSNTILRLSGRVVSVYSVAVVAHALSHLGLCDKSTCTKRVVVPWQLLEBI 424
 Db 366 EQAPMAHTMPKXKAFKSMSSAYNAYRAVVAHGLHQLLGCASGACGRVVPWQLLEQI 425
 QY 425 WKVNFITLHDHJFFDPOGVALHLEIVQWDRSQNPPOSVAS--YYPQROLKNIQDIS 482
 Db 426 HKVHLLHDKDTVAFNDNRDPLSSYNIAIADWNGPKWTFVLGSSSTWSPVQLNI-NETKIQ 484
 QY 483 WHTVNTTIPMSCKRCQSGQKKKGVGHIWCCFECIDCLPGTFLNHTEDYEYCOACPNNE 542
 Db 485 MHGKNQVPSVCSDDCLEGHQHVTVGFHHCFCFCVPCGAGTFLNKS-DLYRCQPCGKEE 543
 QY 543 WYQSETSCFKQLVPLEMHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAGGP 602
 Db 544 WAPESQTCFPRTVVFLALREHTSWVLLAANTLLLLGLTAGLFAWHLDTFVRSAGGR 603
 QY 603 MCFMLMTLLVAVMVVVPVGPVKSTCLCRQALFPLCHFTICISIAVRSFQIVCAFWA 662
 Db 604 LCFMLGSLAAGSGSLYGFGEFTRPACLLRQALFALGETIFLSCITVRSFQIIIFKFS 663
 QY 663 SRFPRAYSVWRYQGPVYSMAFITVLMVIVVIGMLATGLSTTRTPDDPKITIVSCNP 722
 Db 664 TKVPTFYHAWVQNHGAGLFVMISSAAQLLICLTWLVVWTPLP-AREYQRFPLWMLECTE 722
 QY 723 NYRNSL-----LFNTSLDLLSVGVFSFAYNGKELPTNNYNAKFTITLSMTFYFTSSVSL 776
 Db 723 T--NSLGFITLAFYNG-----LLSISAFACSLGKOLPENYNAKCVTFSLLENFVSWIAF 776
 QY 777 CTFMSAYSGVLTVIVDILLVTLNLAISLYGFGPKCYMILFPERTNPAYFNSMIQGYTM 836
 Db 777 FTASVYDGKYLPAANMMAGLSLSSGGYFLPKCYVILCPDLNSTEHFQASIQDYTR 836
 QY 837 R 837
 Db 837 R 837
 RESULT 12
 Q8NGZ7 PRELIMINARY; PRT; 929 AA.
 AC Q8NGZ7
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE Seven transmembrane helix receptor.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Putami K., Matsumoto S.,
 RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB05618; BAC05845.1;
 DR HSSP; P23385; 1IIS.
 DR Genes; HGNC:14448; TAS1R1.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR001828; ANF receptor.
 DR InterPro; IPR000068; Ca_sens receptor.
 DR InterPro; IPR000337; GPCR Mgr.
 DR InterPro; IPR011500; NCD3G_GPCR.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR Pfam; PF07562; NCD3G; 1.
 DR PRINTS; PR00592; CASENSINGR.
 DR PRINTS; PR00248; GPCRMRG.
 DR PROSITE; PS02529; G_PROTEIN_RECEP_F3_4; 1.
 KW Receptor; Transmembrane.
 SQ SEQUENCE 929 AA; 101852 MW; 480FBF67781758654 CRC64;

Query Match 29.0%; Score 1389; DB 2; Length 929;
 Best Local Similarity 36.0%; Pred. No. 9, 1e-87;
 Matches 311; Conservative 130; Mismatches 360; Indels 64; Gaps 18;
 QY 2 GPRAKTICSLPFL-----WLAEPABNSDF-----YLPGLDYLLGGIYFSLHANMK 46
 Db 21 GERA-----SLFLLLSLRLALVEVVMGTGPMTSKVPFAPKPSLGGQVRVAGLCPQLSLT 76
 QY 47 GIVHLNLFQVPMCKEVEKVGICYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDYCIYN 106
 Db 77 GELHRS-----CSNE---HGHLFQAWRLGVEEINNSTALLPMTITGLYQYDYDVCDSA 127
 QY 107 NYQPVLYFLA-----HEDNLLPTQEDYSNYSIRVAVIPDNSESVMTVANFLSLFLLP 162
 Db 128 NYATLRVLSLPQGH---IELQGLLHYSPTVLAVIGPDSTNRAATTAALLSPFLVPMI 184
 QY 163 TVSAISDELDRDKVRFPALLRTPPSADHVEAMVQMLHFRMNIIVLVSSDYGRDNGQL 222
 Db 185 SYAASSETLSVKRQVPSFLRTIPNDKYQVETWVLLQKFGMTWISLVGSSDDYQGLGVQA 244
 QY 223 LGERVARRDICIAFOETLP-TLOPNQNTSEBQRQLVTIVDKLQOSTARVWVVFSPDLTL 281
 Db 245 LENQATGOGICIAFKNDIMPFSQVGD-----ERMQCLMRHLAOGATVWVVFSSRLA 297
 QY 282 YHFFNEVLQRNFTGAVTASBSWAIDPVLHNLTELHGLTFLGITIQSVPIPGFSEFREW 341
 Db 298 RVFFESVVLTLTKGVWVASEAWLSRHTGVPQIGRIQWGLVAVIOKEAVFGLKAFEA 357
 QY 342 GPQA---GPPPLSRFSQSYTCNQCNDCLNATLSPTNLTIRLSGERVWVSVYAVVAHA 398
 Db 358 YARADKAPRCHKGWC-SSNQLCREQCAFMAHTMPKPKAFKSMSSAYNAYRAVVAH 416
 QY 399 LHSLLGCDKSTCTKRVVVPWQLLEBIWKNVTLLDHOIFPDPOGVALHLEIVQWDRS 458
 Db 417 LHQLLGASGACSRGRVVPWQLLEBIQHKVHLLHDKDTVAFNDNRDPLSSYNIAIADWNGP 476
 QY 459 QNPFSQVAS--YYPQLQOLKNIQDISWHTVNTTIPMSCKRCQSGQKKKPVGHIWCCFE 516
 Db 477 KMTFTVLGSSWSPVQLNI-NETKIQNHGKNQVPSVCSDDCLEGHQHVTVGFHHCCE 535
 QY 517 CIDCLPGTFLNHTEDYEYCOACPNNEWSYQSETSCFKQLVPLEWHEAPTIAVALLAALG 576
 Db 536 CVPCGAGTFLNKS-DLYRCQPCGKEWAPESQTCFPRTVVFLALREHTSWVLLAANTLL 594
 QY 577 FLSTLAILVIFWRHFQTPIVRSAGGPMCFMLMTLLVAVMVVVPVGPVKSTCLCRQAL 636
 Db 595 LLLLGLTAGLFAWHLDTFVRSAGGRLCFMLGSLAAGSGSLYGFGEFTRPACLLRQAL 654
 QY 637 FPLCFTICISIAVRSFQIVCAFKMASRFPRAYSVWRYQGPVYSMAFITVLMVIVVIG 696
 Db 655 FALGFTIFLSCITVRSFQIIIFKFTKVPFYHAWVQNHGAGLFVMISSAAQLLICLTW 714
 QY 697 MLATGLSPTRTPDDPKITIVSCNPNYRNSI-----LFNTSLDLLSVGVFSFAYMGK 750
 Db 715 LVVWTPLP-AREYQRFPLWMLECTET--NSLGFITLAFYNG-----LLSISAFACSLGK 767
 QY 751 ELPTNYNEAKFTILSMTPFYFTSSVLSCTFMSAYSGVLTVIVDILLVTLNLAISLYGFGP 810
 Db 768 DLPENYNKACVTFSLLENFVSWIAFTASVYDGKYLPAANMMAGLSLSSGGYFGGYFLP 827
 QY 811 KCMILFYPERNTPAYFNSMIQGYT 835
 Db 828 KCVILCFPDLNSTEHFQASIQDYT 852
 RESULT 13
 Q8TDJ9 PRELIMINARY; PRT; 763 AA.
 ID Q8TDJ9
 AC Q8TDJ9
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE Gm148 form B.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21888635; PubMed=11891061;
 RA Makalowska I., Sood R., Faruque M.U., Hu P., Robbins C.M.,
 RA Eddings E.M., Mestre J.D., Baxevanis A.D., Carpten J.D.,
 RT Identification of six novel genes by experimental validation of
 RT GeneMachine predicted genes."
 RL Gene 284:203-213 (2002).
 DR EMBL; AF387618; AAL91359.1; -.
 DR HSP; P23385; 11SS.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008677; F:metabotropic glutamate, GABA-B-like recepto. .; IEA.
 DR InterPro; IPR001828; ANF_receptor.
 DR InterPro; IPR000068; Ca_sens_receptor.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR InterPro; IPR011500; NCD3G_GPCR.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR PRINTS; PR00592; CASSENSINGR.
 DR PRINTS; PR00248; GPCR_MGR.
 DR PROSITE; PS02059; G_PROTEIN_RECEP_F3_4; 1.
 SQ SEQUENCE 763 AA; 84427 MW; 593616575D6BD17D CRC64;
 Query Match 28.2%; Score 1251; DB 2; Length 763;
 Best Local Similarity 37.0%; Pred. No. 4.7e-84;
 Matches 288; Conservative 124; Mismatches 331; Indels 36; Gaps 13;
 QY 75 MRFAVEINSSLLPGLVGLVYDVCYISNVQPVLYFLA----HEDNLLPIQEDYSN 130
 DB 1 MRLGVEEINSSALLPGLVGLVYDVCYISNVQPVLYFLA----HEDNLLPIQEDYSN 130
 QY 131 YISRVAVIGPDNSVMTVANFLSLPILPOTIYSALISDELDRKVRPALLRTTPSADH 190
 DB 58 YSPVTLAVIGPDNSTRAATTAALLSPFLVPMISVAASSETLSVKRQPSFLRTIPNDKYQ 117
 QY 191 VEAMVQLMHLRPNWIIVLVSSDYGRDNGQLGERVARRDICAFOETLP-TLOPNQNM 249
 DB 118 VETVLLVLLQKFGMTWISLVGSSDDYQGLVQALENQATGQICIAFDIMPFSAQVGD-- 175
 QY 250 TSEERQRLVTVLQLOSTARVVVVFSPDLTLHYFFNEVLQRNFTGAVWIASEWALDPV 309
 DB 176 -----ERNQCLMRHLAAGATVVVVFSSRQLARVFFESVLTNTLTKGVWASEAWLSRH 230
 QY 310 LHLNLTGLHGLTFLGITIQSVIPFGSEFFREWGPOA---GPPPLSRTSQSVTCNQCDC 366
 DB 231 ITGVPGIQRIGWLVGVALQRAVPLGKAFEEAYARADKAPRCHKGSWC--SSNQLCREC 289
 QY 367 LNATLSFNTILRSGRVVSVYSAVAVAHLSLGLCDKSTCTKRVVFWQLLEIWK 426
 DB 290 QAFMAHTMPKLFKAFMSNAYNAVAVAVAHGLHQLLGCASGACSRGRVFWQLLEIHK 349
 QY 427 VNFLLDHLQIFDPQGVVALHLEIVQWDRSQNPFGQVAS--VYPLQRLQKNIQDISWH 484
 DB 350 VHFLLKDTVAFNDRPDLSSYLIANDWNGPKTFFVLGSSVSPQLNT-NETKIQWH 408
 QY 485 TVNNTIPMSCKRCQSGQKKPVGHVCCPECIDCLPGTFLNHTEDBYEQACAPNNEWS 544
 DB 409 GKDNQVPSKVCSSDCLGHQRVAVGFHCCPECVPCGAGTFLNKS-DLYRCQPCGKEWA 467
 QY 545 YQSETSCFKROLVLEWEHEAPTIALLAALGFLSTLAILVIFWEHFTPTIVRSAGGPMC 604
 DB 468 PEGSQTCPRTVVFVLAUREHTSWVLAAANTLILLLLGLTAGLFAWLLDTPVRSAGGRLC 527
 QY 605 FLMLTLILVAVWVPVGGPKVSTCLCRQALFPLCLCTICISIAVRSFQIVCAFWASR 664
 DB 528 FLMLGSLAAGSGSLGYFFXEPTRPACILRQALFALGFTIFLSCLTVRSFQLIILFKFTK 587
 QY 665 FFRAYSVWRYQGPVSVMAFTVTLKMWIIVIGMLATGLSPTRTDDPKITIVSCNPY 724

DB 588 VPTFYHAWQNHGAGLFWMISSAAQLLICLTWLVVMTPLP-AREYQRFPHLVMLECTET- 645
 QY 725 RNSL-----LFNTSLDLLSVVGFSPAYMGKSLPTNYNEAKFTTILSMTFFFTSSVSLCT 778
 DB 646 -NSLGLFILAFLYNG----LLSISAFACSYLGKDLPENYNEAKCVTSLLFNFSVWIAFFT 700
 QY 779 FMSAYSGVLVTIVDLAVTLNLLAISIGYFGPKCYMILFYPERNTPAYFNSMIQGYTMR 837
 DB 701 TASVDGKYLPAANMMAGLSLSSGGFYLPKCYVILCRPDINSTEHFQASIQDYTRR 759
 RESULT 14
 Q8J104 PRELIMINARY; PRT; 1027 AA.
 AC Q8J104; 2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Calcium polyvalent cation receptor/salinity sensing protein.
 OS Squaleus acanthias (Spiny dogfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squala; Hypnosqualea; Squaliformes; Squaloidei;
 OC Squalidae; Squaleus.
 OX NCBI_TaxID=7797;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22103704; PubMed=12093923;
 RA Nearing J., Betka M., Quinn S., Hentschel H., Elger M., Baum M.,
 RA Bai M., Chattopadhyay N., Brown E.M., Hebert S.C., Harris H.W.;
 RT "Polyvalent cation receptor proteins (CaRs) are salinity sensors in
 RT fish."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:9231-9236 (2002).
 DR EMBL; AF406649; AAM77700.1; -.
 DR HSP; P23385; LEWK.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008677; F:metabotropic glutamate, GABA-B-like recepto. .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR001828; ANF_receptor.
 DR InterPro; IPR000068; Ca_sens_receptor.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR InterPro; IPR011500; NCD3G_GPCR.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR Pfam; PF07562; NCD3G; 1.
 DR PRINTS; PR00592; CASSENSINGR.
 DR PRINTS; PR00248; GPCR_MGR.
 DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
 DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; UNKNOWN_1.
 DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
 DR PROSITE; PS02059; G_PROTEIN_RECEP_F3_4; 1.
 KW RECEPTOR.
 SQ SEQUENCE 1027 AA; 114412 MW; 189FF1E123B5B7C7 CRC64;
 Query Match 24.5%; Score 1089; DB 2; Length 1027;
 Best Local Similarity 31.1%; Pred. No. 7.6e-72;
 Matches 278; Conservative 161; Mismatches 360; Indels 96; Gaps 26;
 QY 5 AKTICSLFFLLVLAEPFAENSDFYLP-----CDYLLGLGLSLHANM--KGIVHLNPLQ 55
 DB 2 AQLHCQLLGLFTLLQ--SYNVSGYGNQRAQKGDIIILGLFPFHFGVAAKQDLKGRPE 60
 QY 56 VPMCKEYEVKVIYGLNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVC-YISNNVQPVLYF 114
 DB 61 ATKIRYNFR--GFRWLQAMIFAEIEINNSMTFLNPLTLGYRIEDTCTNTVSKALEATLSF 118
 QY 115 LA-HEDNLLPIQE--DYSNISRVVAVIGPDNSVMTVANFLSLPILPOTIYSALISDEL 171
 DB 119 VAQNKIDSLNLDDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFIPQVSYASSRLL 178
 QY 172 RDKVRFALLRTTFSADHVEAMVQLMHLRPNWIIVLVSSDTYGRDNGQLGERVARRD 231

Db 179 SNKNEYKFLRTPNDPEQQAAMAEIIEHFQWNVGTTLAADDYGRPGIDKFEBAVKRD 238
Qy 232 ICIAQETILPTLPQNMTSEBQRLVTVDKLQOSTARVVVVFSPDLTLHYFFNEVLQ 291
Db 239 ICIDSEMI-----SQYTF--OKQLEFIADVIQNSAKVIVVFGNGPDLEPLIOEIVRR 290
Qy 292 NPTGAVMTASESWAIDPVHLNLTGLTFLGIIQSVPIPGFSEFRE----- 340
Db 291 NITDRWLASEAWASSLLIAKPEYHVVGTTGFALRAGRIFGFKFLKEVHPSSSDNG 350
Qy 341 -----W-----GPOA-GPPPLSRTSQSYTCNQECNCLNAT 370
Db 351 FVKEFEWETFCYFTEKTLTLQKNSKVPESHGPAAGQDGSKAGNSRRRTALRHCHTGEENIT 410
Qy 371 LSFNTILRLSGERVVYSYAVYVAHALHSLGCDKST-----CTK-RVYVPWOLLE 422
Db 411 SVETPYLDYTHLRISYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAWOVLN 470
Qy 423 EIWKNVFT-LLDHQIFFDQGDVALHLEIVQWDRSQNP--FQSVASY-----YPLQRL 475
Db 471 HLLHLKFTNSMGQVDFDDQGLKGNYYIINWQLSAEDESULFHEVGNVNAVAKESDRLN 530
Qy 476 KNIQDISMHTVNTIPMSMCKRSQSGQKKPV-GIHVCCFECIDCLPGLTFLNHTEDYE 534
Db 531 INEKKILSGFKSVVFFNSRDCVPGTRKGIIEGPTCCPECMACAEGEF-SDENDASA 589
Qy 535 COACNNNSYQSETSCPKRQLVLEWHEAPTIIVALLAALGFLSTLAILVFWHFQTP 594
Db 590 CTKCNDPWSNENHTSAKEIYLSWTEPFGIALTIFAVLGILITSFVLGVFIKFRNTP 649
Qy 595 IVRSAGGCMFLMLTLVAVVWVVPVYVGGPKVSTCLCRQALFPLCFTICISCIIVRSPQ 654
Db 650 IVKATNRELSYLLLSLCCFSSSIFIGEPDWTCLRLQAPAGISFVLCISILVKNTR 709
Qy 655 IVCAFMASSRPRA-YSYVWRYQGPVSMAPITVLKMWIWTGMLATGLSPTRTDPDP 713
Db 710 VLLVPE--AKIPTSLSHRKWGLNLQFL-LVFLCILVQIVTCIIWLVAPPSSYRNHELED 766
Qy 714 KITIVSCNPNRNSLLENTSLDLISVGVFSYAYMGKELPTYNKAKPITLSMTFFYFSS 773
Db 767 EVIFITCDGSLMALGFLIGYTCLLAAICFFPFAFKSRKLPENFNKAKTIFTSMLIFFIV 826
Qy 774 VS-LCTFMSAYSGVLVTVTDLLVTVLNLALISGLVFG---PKCYMILFYPERN 823
Db 827 ISFIPAYSTY-GKFSVAE-----VIALASSFGLLGCIYFNKCYIILFKPCRN 876
RESULT 15
CASR HUMAN
ID CASR HUMAN STANDARD; PRT: 1078 AA.
AC P41180; Q13912; Q16108; Q16109; Q16110; Q16379;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid
Cell calcium-sensing receptor)
GN Name=CASR; Synonyms=GPRC2A, PCAR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Pearce S.H.S., Thakker R.V.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Parathyroid;
RX MEDLINE=95279439; PubMed=7759551;
RA Garrett J.B., Capuano I.V., Hammerland L.G., Hung B.C., Brown E.M.,
RA Hebert S.C., Nemeth E.F., Fuller F.;
RT "Molecular cloning and functional expression of human parathyroid
calcium receptor cDNAs.";

J. Biol. Chem. 270:12919-12925(1995).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=95408281; PubMed=7677761;
RA Aida K., Koishi S., Tawata M., Onaya T.;
RT "Molecular cloning of a putative Ca(2+)-sensing receptor cDNA from
human kidney";
RL Biochem. Biophys. Res. Commun. 214:524-529(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=96343808; PubMed=8756555;
RA Freichel M., Zink-Lorenz A., Hollsch A., Hafner M., Flockerzi V.,
RA Raue F.;
RT "Expression of a calcium-sensing receptor in a human medullary thyroid
carcinoma cell line and its contribution to calcitonin secretion";
RL Endocrinology 137:3842-3848(1996).
RN [5]
RP SEQUENCE OF 643-908 FROM N.A.
RX MEDLINE=96193893; PubMed=8613532;
RA Bikle D.D., Ratnam A., Mauro T., Harris J., Pillai S.;
RT "Changes in calcium responsiveness and handling during keratinocyte
differentiation. Potential role of the calcium receptor.";
RL J. Clin. Invest. 97:1085-1093(1996).
RN [6]
RP VARIANTS FHH GLN-185; LYS-297 AND TRP-795.
RX MEDLINE=94094324; PubMed=7916660;
RA Pollak M.R., Brown E.M., Chou Y.-H.W., Hebert S.C., Marx S.J.,
RA Steinmann B., Levi T., Seidman C.B., Seidman J.G.;
RT "Mutations in the human Ca(2+)-sensing receptor gene cause familial
hypocalcemic hypercalcemia and neonatal severe hyperparathyroidism.";
RL Cell 75:1297-1303(1993).
RN [7]
RP VARIANT ADH ALA-127.
RX MEDLINE=95179179; PubMed=7874174;
RA Pollak M.R., Brown E.M., Estep H.L., McLaine P.N., Kifor O., Park J.,
RA Hebert S.C., Seidman C.B., Seidman J.G.;
RT "Autosomal dominant hypocalcaemia caused by a Ca(2+)-sensing receptor
gene mutation.";
RL Nat. Genet. 8:303-307(1994).
RN [8]
RP VARIANTS FHH MET-62; CYS-66; MET-138; GLU-143 AND GLN-227.
RX MEDLINE=95243222; PubMed=7726161;
RA Chou Y.-H.W., Pollak M.R., Brandi M.L., Toss G., Arnqvist H.,
RA Atkinson A.B., Papadoulos S.E., Marx S., Brown E.M., Seidman J.G.,
RA Seidman C.B.;
RT "Mutations in the human Ca(2+)-sensing-receptor gene that cause
familial hypocalcemic hypercalcemia";
RL Am. J. Hum. Genet. 56:1075-1079(1995).
RN [9]
RP SEQUENCE OF 1-61 FROM N.A., AND VARIANT FHH ALA-39.
RX MEDLINE=95403641; PubMed=7673400;
RA Aida K., Koishi S., Inoue M., Nakazato M., Tawata M., Onaya T.;
RT "Familial hypocalcemic hypercalcemia associated with mutation in the
human Ca(2+)-sensing receptor gene";
RL J. Clin. Endocrinol. Metab. 80:2594-2598(1995).
RN [10]
RP VARIANTS NSHPT LEU-227 AND TYR-582.
RX MEDLINE=96292293; PubMed=8675635;
RA Pearce S.H.S., Trump D., Wooding C., Besser G.M., Chew S.L.,
RA Grant D.B., Heath D.A., Hughes I.A., Paterson C.R., Whyte M.P.,
RA Thakker R.V.;
RT "Calcium-sensing receptor mutations in familial benign hypercalcemia
and neonatal hyperparathyroidism";
RL J. Clin. Invest. 96:2683-2692(1995).
RN [11]
RP VARIANTS FHH THR-116; HIS-681 AND SER-806, AND VARIANT SER-851.
RX MEDLINE=96311554; PubMed=8733126;
RA Baron J., Winer K.K., Yanovski J.A., Cunningham A.W., Laue L.,
RA Zimmerman D., Cutler G.B. Jr.;
RT "Mutations in the Ca(2+)-sensing receptor gene cause autosomal
dominant and sporadic hypoparathyroidism";
RL Hum. Mol. Genet. 5:601-606(1996).

RN [12] MEDLINE=97442275; PubMed=9298824;
 RP VARIANT FHH ARG-174.
 RA Ward B.K., Stuckey B.G.A., Gutteridge D.H., Laing N.G., Pullan P.T.,
 RA Ratajczak T.;
 RT "A novel mutation (L174R) in the Ca2+-sensing receptor gene associated
 RT with familial hypocalcemic hypercalcemia.";
 RL Hum. Mutat. 10:233-235(1997).
 [13]
 RP VARIANT FHH VAL-616
 RX MEDLINE=99415602; PubMed=10487661;
 RA Stock J.L., Brown R.S., Baron J., Coderre J.A., Mancilla E.,
 RA De Luca F., Ray K., Mericq M.V.;
 RT "Autosomal dominant hypoparathyroidism associated with short stature
 RT and premature osteoarthritis.";
 RL J. Clin. Endocrinol. Metab. 84:3036-3040(1999).
 [14]
 RP VARIANT FHH GLU-557.
 RX MEDLINE=21603857; PubMed=11762699;
 RA Nakayama T., Minato M., Nakagawa M., Soma M., Tobe H., Aoi N.,
 RA Kosegawa K., Sato M., Ozawa Y., Kamatsuse K., Kokubun S.;
 RT "A novel mutation in Ca2+-sensing receptor gene in familial
 RT hypocalcemic hypercalcemia.";
 RL Endocrine 15:277-282(2001).
 CC -!- FUNCTION: Senses changes in the extracellular concentration of
 CC calcium ions. The activity of this receptor is mediated by a G-
 CC protein that activates a phosphatidylinositol-calcium second
 CC messenger system.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P41180-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P41180-2; Sequence=VSP_002035;
 CC -!- TISSUE SPECIFICITY: Found in kidney, but not in brain, lung,
 CC liver, heart, skeletal muscle, or placenta.
 CC -!- DISEASE: Defects in CASR are the cause of familial hypocalcemic
 CC hypercalcemia, type 1 (FHH) [MIM:145980]; in which the receptor
 CC has reduced activity. FHH is characterized by altered calcium
 CC homeostasis. Affected individuals exhibit mild or modest
 CC hypercalcemia, relative hypocalcemia, and inappropriately normal
 CC PTH levels.
 CC -!- DISEASE: Defects in CASR are the cause of neonatal severe primary
 CC hyperparathyroidism (NSHPT) [MIM:239200]; in which the receptor
 CC has reduced activity. NSHPT is a rare autosomal recessive life-
 CC threatening disorder characterized by very high serum calcium
 CC concentrations, skeletal demineralization, and parathyroid
 CC hyperplasia. In some instances NSHPT has been demonstrated to be
 CC the homozygous form of FHH.
 CC -!- DISEASE: Defects in CASR are the cause of autosomal dominant
 CC hypocalcemia (ADH) [MIM:601198]; in which the receptor is
 CC activated at subnormal Ca(2+) levels.
 CC -!- DISEASE: Defects in CASR are the cause of autosomal dominant
 CC hypoparathyroidism (FHH) [MIM:146200]. FHH is characterized by
 CC hypocalcemia and hyperphosphatemia due to inadequate secretion of
 CC parathyroid hormone. Symptoms are seizures, tetany and cramps.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor family 3.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X81086; CRA56990.1; -;
 DR EMBL; U20759; AAA86503.1; -;
 DR EMBL; U20760; AAA86504.1; -;
 DR EMBL; D50855; BAA09453.1; -;
 DR EMBL; S83176; AAB46873.1; -;
 DR EMBL; S79217; AAB35262.2; -;

DR EMBL; S68032; AAB29413.2; ALT_SEQ.
 DR EMBL; S68033; AAB29414.1; -;
 DR EMBL; S68036; AAB29415.1; -;
 DR EMBL; S81755; AAD14370.1; -;
 DR HSP; P23385; IHWK.
 DR Genew; HGNC:1514; CASR.
 DR MIM; 601199; -;
 DR MIM; 145980; -;
 DR MIM; 239200; -;
 DR MIM; 601198; -;
 DR MIM; 146200; -;
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0004930; F: G-protein coupled receptor activity; TAS.
 DR GO; GO:0004435; F: phosphoinositide phospholipase C activity; TAS.
 DR GO; GO:0006874; P: calcium ion homeostasis; TAS.
 DR GO; GO:0005513; P: calcium ion sensing; TAS.
 DR GO; GO:0007635; P: chemosensory behavior; TAS.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signaling; TAS.
 DR GO; GO:0009653; P: morphogenesis; TAS.
 DR GO; GO:0001503; P: ossification; TAS.
 DR InterPro; IPR001828; ANF receptor.
 DR InterPro; IPR000068; Ca sens. receptor.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR Pfam; PF00003; 7tm_3; 1.
 DR PRINTS; PR00248; GPCRMR.
 DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
 DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
 DR PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.
 Query Match 24.3%; Score 1079.5; DB 1; Length 1078;
 Best Local Similarity 31.4%; Pred. No. 4.1e-71;
 Matches 279; Conservative 160; Mismatches 342; Indels 107; Gaps 27;
 Qy 16 WVLAEPAENSDVLP-----GDYLLGLFSLHANMKGIVHLNLFQVPMCKEYEVKVG 68
 Db 8 WVLALTWHTSAYGPDQRAQKGGIILGGLPIHF---GVAAKD--QDLKSRPSEVCEIR 62
 Qy 69 YNL-----MQAMFAVEEINNDSSLLPGVLLGVEIVDVC-VISNNVOPVLYFLA-HBDNL 121
 Db 63 YNFRGFWLQAMFAIEEINSSPALLNLTLGTRIFDTCTVSKALATLSFVAQNKIDS 122
 Qy 122 LPIQE--DYSNYSRVVAVIPDNSESVMVTANFLSLFLPQITYSAISDELDRDKVPPA 179
 Db 123 LNLDFCNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSRLLSNKQFKS 182
 Qy 180 LLRTTPSADHVEAMVQMLHFRNWIIVLVSSDTCGRDNGQLLGERVARRDICTAQET 239
 Db 183 FLRTIPNDEHQATAMADIIEYFRNWNVGTIAADDDYGRPGIEKPREAEERDICI DPFSEL 242
 Qy 240 LPTLQPNQNMTSBERQRLVTIVDKLQOSTARVVVVFSPDLTLVHFFNEVLRFQNTGAVWI 299
 Db 243 I-----SQYDEBEI QHVVEVI---QNSTAKVIVFSSGPDLEPLIKEIVRNTIGKIWL 294
 Qy 300 ASESWAIDPVHLNLTGLHGTFLGIFTIQSVIPGPSEF-----REWGPQ 344
 Db 295 ASEAWASSSLIAMPQYPHVVGGTGTGFAKAGQIPGPFREFLKKVHKPRKSVHNGFAKEPWE 354
 Qy 345 A-----GPPLSRTSQSYTCNQCENCLNATLSNTILSLGE----- 382
 Db 355 TFNCHLOEAGKGLPVDVTFRLGH--EESGRFNSSTAFRPL--CTGDNISSVETPYID 410
 Qy 383 ---RVVYSVYSVAVVAHAHSLGCG-----DKSTCTKRVVYVPWQLLEETIKVNF 430
 Db 411 YTHLRISVNVYLVYSTAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKHLRLHFT 470
 Qy 431 -LDHQITFPDQGVNHLHLEIVQMWRDSONP--FQSVASYPL-----ORQLXNIQDIS 482
 Db 471 NNMGEQVTFDECDGLVNGYIINWHLSPEDGSIYFKEV-GYINYVYAKKGERLFTNEEKIL 529
 Qy 483 WHTVNTNTPMSCKSKRCQSGKKPV-GIHVCCPECIDCLPGTFLNHTDEVEYEQACPN 541

Db 530 WSGFSREVPFNSCRDCLAGTRKGIIEGBPTCCFECVECPDGEYSDET-DASACNKCDD 588
QY 542 EMSYQSETSCFKRQLVLEWHEAPTIATAVALLAALGFLSTLAIIVIFWRHFQPIVRSAGG 601
Db 589 FWSNENHTSCIAKEIEFLEWTEPFGIALTLFAVLGIFLTAFLGVFIKFRNTPIVKAATR 648
QY 602 PMCFLMLTLLLVAYMVVPPVYVGPVKVSTCLCRQALFPLCFTTICISCIAYRSFQIVCAP-- 659
Db 649 ELSYLLLFSLCCFSSSLFFIGEPQDWTCLRQPAFGISFVLCISCLVKTNRVLLVFEA 708
QY 660 KMASRFPRAYSWVRVQGPVVSMAFITVLKMWIVWIGMLATGLSPTRTDDDDPKITIVS 719
Db 709 KIPTSPHRK---WMLNLOFLLVFLCTFMQIVICVI-WLYTAPPSSYRNQOELEIIFIT 764
QY 720 CNPNYRNSLLENTSLDLLSVVGFSPAYMGKELPTNYNEAKFTILSMFTFYFTSSVSLCTF 779
Db 765 CHEGSLMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFTIFSMLIFFIVWIS---F 821
QY 780 MSAYSGVLVTIVDLLVTVNLNLAISLG---YFGPKCYMILFYPERNT 823
Db 822 IPAYASTYGFVS-AVEVIAILAASFGLLACIFFNKIYIILKPSSENT 868

Search completed: November 30, 2004, 13:54:51
Job time : 213 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 30, 2004, 13:45:48 ; Search time 45 Seconds
(without alignments)
1793.908 Million cell updates/sec

Title: US-10-035-045-21

Perfect score: 4443

Sequence: 1 MGPRAKTICSUFFLLWLAE.....ERNTPAYFNSMIQGYTMRD 839

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1079.5	24.3	1078	2 A56715	calcium receptor (
2	1075	24.2	1079	2 I53362	calcium/polyvalent
3	1075	24.2	1085	2 S40476	Ca(2+)-sensing rec
4	1064.5	24.0	1088	2 B56715	calcium receptor (
5	1014.5	22.8	858	2 JC7683	taste receptor T1R
6	730	16.4	915	2 A49874	metabotropic gluta
7	720.5	16.2	879	2 JC7160	metabotropic gluta
8	720.5	16.2	879	2 JH0562	metabotropic gluta
9	714	16.1	912	2 JH0563	metabotropic gluta
10	699	15.7	872	2 JH0561	metabotropic gluta
11	682.5	15.4	1171	2 A42916	metabotropic gluta
12	673	15.1	1180	2 JC2132	metabotropic gluta
13	673	15.1	1212	2 JC2131	metabotropic gluta
14	668.5	15.0	871	2 A46742	metabotropic gluta
15	668.5	15.0	908	2 I49142	metabotropic gluta
16	656	14.8	999	2 T27628	metabotropic gluta
17	653.5	14.7	1199	2 A41939	G protein-coupled
18	648.5	14.6	1218	2 T31376	glutamate receptor
19	632	14.2	1267	2 T21340	hypothetical prote
20	425.5	9.6	551	2 T30806	metabotropic gluta
21	218.5	4.9	921	2 T31136	ionotropic glutama
22	218.5	4.9	923	2 F84732	probable ligand-ga
23	215	4.8	1039	2 T45779	probable glutamate
24	200.5	4.5	953	2 E84732	probable ligand-ga
25	200	4.5	1099	2 T16283	hypothetical prote
26	186	4.2	950	2 T31134	ionotropic gluta
27	185.5	4.2	925	2 T06128	hypothetical prote
28	185	4.2	975	2 A84550	probable ligand-ga
29	184	4.1	925	2 T51133	ligand gated chann

30	184	4.1	951	2 T51132	probable glutamate
31	180	4.1	960	2 JE0356	gamma-aminobutyric
32	177.5	4.0	1005	2 S33525	guanylate cyclase
33	176	4.0	933	2 C96495	probable ligand-ga
34	174.5	3.9	912	2 T51131	ligand-gated chann
35	169.5	3.8	941	2 T51135	ligand-gated chann
36	168.5	3.8	962	2 D86186	hypothetical prote
37	160.5	3.6	1679	2 T15968	hypothetical prote
38	158.5	3.6	976	2 T51137	ionotropic glutama
39	158	3.6	997	2 S33754	glutamate receptor
40	144	3.2	918	2 I58178	glutamate receptor
41	144	3.2	949	2 S19808	glutamate receptor
42	143	3.2	965	2 I51244	N-methyl-D-asparta
43	131.5	3.0	1125	1 OYURCP	speract receptor p
44	130.5	2.9	938	2 A46612	N-methyl-D-asparta
45	129.5	2.9	885	2 JN0339	N-methyl-D-asparta

ALIGNMENTS

RESULT 1

A56715
calcium receptor (clone phpCar-4.0) - human
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence revision 19-Oct-1995 #text_change 01-Dec-2000
C:Accession: A56715; S49341; A49419; B49419; C49419
R:Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.C
J. Biol. Chem. 270, 12919-12925, 1995
A:Title: Molecular cloning and functional expression of human parathyroid calcium recept
A:Reference number: A56715; MUID:95279439; PMID:7759551
A:Accession: A56715
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-1078 <GAR>
A:CROSS-references: GB:U20759; NID:g683744; PIDN:AAA86503.1; PID:g683745
R:Pearce, S.H.S.; Thakker, R.V.
submitted to the ENBL Data Library, August 1994
A:Reference number: S49341
A:Accession: S49341
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-180,'Q',182-989,'R',991-1078 <PEA>
A:CROSS-references: ENBL:X81086
R:Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi,
Cell 75, 1297-1303, 1993
A:Title: Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalciuri
A:Reference number: A49419; MUID:94094324; PMID:7915660
A:Accession: A49419
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 178-192 <POL>
A:Experimental source: family N
A>Note: sequence inconsistent with nucleotide translation
A>Note: sequence modified after extraction from NCBI backbone
A>Note: 186-Arg mutation is associated with familial hypocalciuric hypercalcemia and neon
A>Note: sequence extracted from NCBI backbone (NCBIN:142453)
A:Accession: B49419
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 289-303 <PO2>
A:Experimental source: family E
A>Note: sequence modified after extraction from NCBI backbone
A>Note: 298-Lys mutation is associated with familial hypocalciuric hypercalcemia and neon
A>Note: sequence extracted from NCBI backbone (NCBIN:142455)
A:Accession: C49419
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 788-802 <PO3>
A:Experimental source: family J
A>Note: sequence modified after extraction from NCBI backbone
A>Note: 796-Trip mutation is associated with familial hypocalciuric hypercalcemia and neon
A>Note: sequence extracted from NCBI backbone (NCBIN:142457)

C:Keywords: glycoprotein; receptor; transmembrane protein

Query Match 24.3%; Score 1079.5; DB 2; Length 1078;
 Best Local Similarity 31.4%; Pred. No. 1.8e-73; Indels 107; Gaps 27;
 Matches 279; Conservative 160; Mismatches 342;
 QY 16 WLLAEPNEDFYLP-----GDYLLGLFSLHNMKGIVHLNLFLOVPCKEYEVKVG 68
 DB 8 WLLALTWHTSAVGPQDQRAQKGGDILGLGLPIHF---GVAKD--QDLKSRPESVEICR 62
 QY 69 YNL-----MQAMFAVEEINNDSSLLPGVLLGVEIVDVC--YISNNVQVLYFLA-HEDNL 121
 DB 63 YNFRGFWLQAMFAIBEINSPLLNLTGRIYFDTCNTVSKALEATLSFVAQNKIDS 122
 QY 122 LPTQE--DYSNYLSRVAVTGPDSVMTVANFLSLFLPLQIYSAISDELDRKKVFEPA 179
 DB 123 LNDLFCNCESEHIPSTTAVGATGSGVSTAVANLLGLFYIQVSYASSRLLSNQFKS 182
 QY 180 LLRTTPGADHHVEAMVQMLHFRNNWIIIVLSSDTYGRDNGQLLGERVARRDICIAPQET 239
 DB 183 FLRTIPNDEHQATAMADIIEYFRNNWVGTIAADDDYGRPGIEKPREAEERDICIAPSEL 242
 QY 240 LPTLPQNMNTSHERQLVTIVDKLQOSTARVVVFPSPDLTLHYHFNELVRONFTGAVMI 299
 DB 243 I-----SQYDSEEEIQHVVEVI---QNSTAKVIVVSSGPDPLEIKIIVRNNITGKIWL 294
 QY 300 ASWSMAIDPVLHNLTELGLTGLGITIQSVPIPGPSEF-----REWGPO 344
 DB 295 ASEAWASSLLAMPQYHVHVGTTGPAKAGQIPGFREFLKKVPRKSVHNGFAKEFTEE 354
 QY 345 A-----GPPPLSRTSQSYTCNCECNCLNATLSFNTILRSGE----- 382
 DB 355 TFNCHLOQAGKGLPVDTFLRGH--BESGRFSNSTAFRPL--CTGDNISSEVETPYID 410
 QY 383 -----RVVYSVYSAVVAHAHLSLGC-----DKSTCKRVVYVQWLLLEEIKWNFT 430
 DB 411 YTHLRISYVYLVAVYSIAHALQDIYTCPLPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFT 470
 QY 431 -LLDHOIFEDPQGDVALHLEIVQWDRSQNP--FQSVASYPL-----QROLKNIODIS 482
 DB 471 NNMGQVTFDECGLDVGNYSLIINHLSPEDGSIYFKEV-GYNNVYAKKGERLFINEEKIL 529
 QY 483 WHTVNNTPMSKCRQSGQKKPV-GIHVCCFECIDCLPGTFLNHTEDYEQACPNN 541
 DB 530 WSGFSREVFPSCSRDCLAGTRKGIIEGPTCCFCEVCEPDGYSDET-DASACNKPDD 588
 QY 542 EWSVQSTSCPKROLVFLHEHATIAVALLAALGFLSTLAILVIFWRHFTPTVRSAGG 601
 DB 589 FWSNENHTSCIAKIEFLSWTEPFGLIALTLFAVLGIFLTAFLVGLVFIKFRNTPIVKATNR 648
 QY 602 PMCFMLTLTLLVAVMVVYVGPVKVSTCLCRQALFPLCFCTICISCIARSFQIVCAF-- 659
 DB 649 ELSVILLFSLCCSSSLFFIGEQDWTCLRQAFGISFVLCISCLIVKTNRLVLLVEA 708
 QY 660 KMASRFPRAVSYWRYQGYVMAFITVLMVIVIGMLATGLSPTTRTDPPDKITIVS 719
 DB 709 KIPTSFHRK--WNLNLQFLVFLCTFMQIVCVI-WLYTAPPSSYRNQELDEIIFIT 764
 QY 720 CNPNYRSLNTSLDILLVSVGFSYAMGKELPNTYNEAKFITLSMTFYTSVSLCTF 779
 DB 765 CHEGSLMALGLFIYGTCLLAAICFFFAFKSRKLPENFNEAKFITPSMLIFFIVMIS---F 821
 QY 780 MSAYSGVLVTVDLLVNLNLALSLG----YFGPKCYMILFYPERNT 823
 DB 822 IPAVASTYKGKFS-AVEVIALAASFGLLACIFFNKIYIILFKPSRNT 868

RESULT 2

159362

calcium/polyvalent cation-sensing receptor precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: 159362; A55594

R;Ruot, M.; Molliver, M.E.; Snowman, A.M.; Snyder, S.H.
 Proc. Natl. Acad. Sci. U.S.A. 92, 3161-3165, 1995
 A;Title: Calcium sensing receptor; molecular cloning in rat and localization to nerve to
 A;Reference number: 159362; MUID:95241465; PMID:7724534
 A;Accession: 159362
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-1079 <RES>
 A;Cross-references: UNIPROT:P48442; EMBL:U20289; NID:g790578; PID:AAC52195.1; PID:g790
 R;Riccardi, D.; Park, J.; Lee, W.S.; Gamba, G.; Brown, E.M.; Hebert, S.C.
 Proc. Natl. Acad. Sci. U.S.A. 92, 131-135, 1995
 A;Title: Cloning and functional expression of a rat kidney extracellular calcium/polyval
 A;Reference number: A55594; MUID:95116508; PMID:7816802
 A;Accession: A55594
 A;Molecule type: mRNA
 A;Residues: 1-133, 'X', 135-1079 <RIC>
 A;Cross-references: GB:U10354
 C;Keywords: calcium; glycoprotein; phosphoprotein; transmembrane protein
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;187-212/Region: hydrophobic
 F;613-635/Domain: transmembrane #status predicted <TM1>
 F;650-670/Domain: transmembrane #status predicted <TM2>
 F;683-700/Domain: transmembrane #status predicted <TM3>
 F;725-744/Domain: transmembrane #status predicted <TM4>
 F;770-790/Domain: transmembrane #status predicted <TM5>
 F;806-828/Domain: transmembrane #status predicted <TM6>
 F;841-860/Domain: transmembrane #status predicted <TM7>
 F;90,261,287,386,468,488,594,893,1005/Binding site: carbohydrate (Aen) (covalent) #statu
 F;794/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F;899,901/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predic

Query Match 24.2%; Score 1075; DB 2; Length 1079;

Best Local Similarity 31.4%; Pred. No. 4e-73;
 Matches 282; Conservative 166; Mismatches 327; Indels 124; Gaps 33;

QY 10 SLFELLWLAEPNEDFYLP-----GDYLLGLFSLHNMKGIVHLNLFLOVPCKEY 62
 DB 9 ALLALAW-----HSSAYGPDQRAQKGGDILGLGLPIHF---GVAKD--QDLKSRPE 56
 QY 63 EVKVGYNL-----MQAMFAVEEINNDSSLLPGVLLGVEIVDVC--YISNNVQVLYFLA 116
 DB 57 SVCEIRYNGFRWLQAMFAIBEINSPLLNLTGRIYFDTCNTVSKALEATLSFVA 116
 QY 117 -HEDNLPIQE--DYSNYLSRVAVTGPDSVMTVANFLSLFLPLQIYSAISDELDR 173
 DB 117 QNKIDSNLNDEFNCSEHIPSTTAVGATGSGVSTAVANLLGLFYIQVSYASSRLLSN 176
 QY 174 KVRFPALLRTPPSADHHVEAMVQMLHFRNNWIIIVLSSDTYGRDNGQLLGERVARRDIC 233
 DB 177 KNQYKSLRTPNDEHQATAMADIIEYFRNNWVGTIAADDDYGRPGIEKPREAEERDIC 236
 QY 234 IAPQETLTPQNQNMNTSHERQLVTIVDKLQOSTARVVVFPSPDLTLHYHFNELVRONF 293
 DB 237 IDFSLEI-----SQYDSEEEIQHVVEVI---QNSTAKVIVVSSGPDPLEIKIIVRNI 288
 QY 294 TGAVVIASESMAIDPVLHNLTELGH-LGTFLGITIQSVPIPGPSEF----- 338
 DB 289 TGRVWLAESAASSLI-AMPEYHVVGGTIGFGLKAGQIPGFREFLKKVPRKSVHNGF 347
 QY 339 -REWGPOA-----GPPPLSRTSQSYTCNCECNCLNATLSFNTILRSGE----- 382
 DB 348 AKEFWEETFNCHLOQAGKGLPVDTFVRSH--EEGNRLNLSNSTAFRPL--CTGDNINS 403
 QY 383 -----RVVYSVYSAVVAHAHLSLGC-----DKSTCKRVVYVQWLLLEE 423
 DB 404 VETPYMDEHLRISYNNVLAIVYSIAHALQDIYTCPLPGRGLFTNGSCADIKKVEAWQVLKH 463
 QY 424 IWKVNT-LLDHOIFEDPQGDVALHLEIVQWDRSQNP--FQSVASYPL-----QROL 475
 DB 464 LRHLNFTNNMGQVTFDECGLDVGNYSLIINHLSPEDGSIYFKEV-GYNNVYAKKGERL 522

QY 476 KNIQDISWHTVNNITPMSCKRCSQGGKKPV-GIHVCCFBCIDCLPGTFLNHTDEYE 534
 Db 523 INEEKILWGSFREVFNFSNDCQAGTRKGIIEGPTCCFCEVCPCDEYSGET-DASA 581
 QY 535 COACPNNEWSQOSETCFRQLVLEWHEAPTIALLAALGFLSLTALIVLFWRHFTQTP 594
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 Db 642 IVKATNRELSYLLFSLCCFSSSLFFIGEPODWTCLRLQPAFGISFVLCISILVKTNR 701
 QY 655 IVCAFMAKSRFRAY--STW-VRYQPYVSMAPITVLKMWIVVIGMLATGLSPTTRTDDP 711
 Db 702 VLLVEF-AKIPTSFRKMWGLNQ---FLVFLCTFMQILICIIWLVTAPSSVRNHEL 756
 QY 712 DPKITIVSCNPNVNSLLNTSL---DLILSVVGSFAYMGKELPTNYNEAKFITLSWTF 768
 Db 757 EDEIFITC---HEGSMALGSLIGYTCLLAALCFEFAKSKRLPENFNEAKFITFSMLI 813
 QY 769 YFTSSVSLCTFMSAYSGVLVTVLTLVTLNLLAISLG---YFGPKCYMILFYPERNT 823
 Db 814 FRIVWIS---FIPAVASTYKGFVS-AVEVIALAASFGLLACIFPNKVYIILFKPSRNT 868
 RESULT 3
 S40476
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 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S40476
 R:Brown, E.M.; Gamba, G.; Riccardi, D.; Lombardi, M.; Butters, R.; Kifor, O.; Sun, A.; H
 Nature 366, 575-580, 1993
 A:Title: Cloning and characterization of an extracellular Ca(2+)-sensing receptor from h
 A:Reference number: S40476; MUID:94077182; PMID:8255296
 A:Accession: S40476
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1085 <BRO>
 A:Cross-references: UNIPROT:P35384; GB:S67307; NID:9453108; PIDN:AAB29171.1; PID:9453109
 Query Match 24.2%; Score 1075; DB 2; Length 1085;
 Best Local Similarity 31.5%; Pred. No. 4e-73;
 Matches 279; Conservative 161; Mismatches 347; Indels 98; Gaps 29;
 QY 11 LFFLLWLAEPAGNDGYLPQDYLGLGLFSLHANKMGIVHLNFLOVP---MCKEYEVKVI 67
 Db 11 LAFSTWCTSAVGPQDQRAQKKGDIILGLLPIHFGV-AVKDQDKRSPESVEICIRNFR-- 67
 QY 68 GYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVC-YISNNVQPVLYFLA-HEDNLLPTQ 125
 Db 68 GFRWLQAMIFATEEINSPALLPNMTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLND 127
 QY 126 E--DYSNVISRVAVIGPDNSVMTVANFLSLFLLPQITYSASIDELRDKVRFPALLRT 183
 Db 128 EFCNCSHPISTIAVVGATGSGISTAVANLLGLFYIPQVYASSSRLSNKQKFSFLRT 187
 QY 184 TPSADHVEAMVOLMLHFRWNWIIVLVSDTYGRDNGQLLGERVARRDICIATFQTLPTL 243
 Db 188 IPNDEHQATAMADIIEYFRWNWGTIAADDDYGRGIEKFPREAEERDICI DFSLI--- 244
 QY 244 QPNQNTSEERQRLVTIIVDKLQOSTARVVVFPSPDLTYHFFNEVLNQFTGAVWIASES 303
 Db 245 ----SQYSD-EKIQVVEVIQNSTAKVIVFSSGPDLEPLIKEIVRNITGRWLASEA 299
 QY 304 WAIQDVLNHLTELGH-LGTFLGITTSQVPIPGFSEF-----REWQQA-- 345
 Db 300 WASSSLI-AMPEYFHWGVTIGFGLKAGIQPGFREFLOKVRPKSVHNGFAKEFEETFN 358
 QY 346 -----GPPPL-----SRTSOSYI-----CNQECNCLNATLSFNTILRSG 381
 Db 359 CHLQEGAKGPLVDTLFGRHBEGBGRLSNSPTAFPLCTGE-ENISSVETPYMDYTHL-- 415

QY 382 ERVTVSVYSAVYAVAHALHSLGCG-----DKSTCTKRVVVPVQMLLBEIKWKNFTL-L 432
 Db 416 -RISYNYLVAVSIAHALQDIYTCIPGRGLFNGSCADIKKVEAQVXLHRLHNTSNM 474
 QY 433 DHOIFPDPOGVALHLEIVQWQWDRSQNP--FQSVASYIPL-----ORQLKNIQDISWHT 485
 Db 475 GQVTFDECGDLAGNYSIINMHLSPEDGSIVPEKV-GYNNVYAKKGERLFINDEKILWSG 533
 QY 486 VNNTIPMSCKSRCSQGGKKPV-GIHVCCFBCIDCLPGTFLNHTDEYE COACPNNEWS 544
 Db 534 FREVFPNSCSRDCLAGTRKGIIEGPTCCFCEVCPCDEYSDET-DASACDKCPDDFWS 592
 QY 545 YQSETSCFRQLVLEWHEAPTIALLAALGFLSLTALIVLFWRHFTQPIVRSAGGPM 604
 Db 593 NENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIFLFAVLGIFKFRNTPIVKATNRELS 652
 QY 605 FLMTLTLLVAYMVVPPVGGPKVSTCLCRQALFPLCFTICISCIARVSQIVCAF--KMA 662
 Db 653 YLLLSFLLCCFSSSLFFIGEPODWTCLRLQPAFGISFVLCISILVKTNRVLLVFEAKIP 712
 QY 663 SRFPRAYSWVRYQGPYVSMAPITVLKMWIVVIGMLATGLSPTTRTDDPKITIVSCNP 722
 Db 713 TSFHRK---WGLNLQFLLVFLCTFMQIVICAI-WLNTAPSSSYRNHELEDEIIFITCHE 768
 QY 723 NYRNSLLENTSLDLLSVVGSFAYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFMSA 782
 Db 769 GSLMALGFLIGYTCLLAALCFEFAKSKRLPENFNEAKFITFSMLI FFIWIS---FIPA 825
 QY 783 YSGVLVTVLTLVTLNLLAISLG---YFGPKCYMILFYPERNT 823
 Db 826 YASTYKGFVS-AVEVIALAASFGLLACIFPNKVYIILFKPSRNT 869
 RESULT 4
 B56715
 C:Species: Homo sapiens (man)
 C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000
 C:Accession: B56715
 R:Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.C
 J. Biol. Chem. 270, 12919-12925, 1995
 A:Title: Molecular cloning and functional expression of human parathyroid calcium recept
 A:Reference number: A56715; MUID:95279439; PMID:7759551
 A:Accession: B56715
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1088 <GAR>
 A:Cross-references: GB:U20760; NID:9683746; PIDN:AAA86504.1; PID:g683747
 C:Keywords: glycoprotein; receptor; transmembrane protein
 Query Match 24.0%; Score 1064.5; DB 2; Length 1088;
 Best Local Similarity 31.1%; Pred. No. 2.5e-72;
 Matches 279; Conservative 160; Mismatches 342; Indels 117; Gaps 28;
 QY 16 WVLARPAENSDFYLP-----GDYLLGLGLFSLHANKMGIVHLNFLOVP MCKEYEVKVI 68
 Db 8 WVLLALWHTSAVGPDQRAQKKGDIILGLLPIHFGV--GVAKD--QDKRSPESVEICIR 62
 QY 69 YNL-----MQAMRFAVEEINNDSSLLPGVLLGYEIVDVC-YISNNVQPVLYFLA-HEDNL 121
 Db 63 YNFRGRLQAMIFATEEINSPALLPNMTLGYRIFDTCNTVSKALEATLSFVAQNKIDS 122
 QY 122 LPIQES--DYSNVISRVAVIGPDNSVMTVANFLSLFLLPQITYSASIDELRDKVRPFA 179
 Db 123 LNLDFCNCSHPISTIAVVGATGSGVSTAVANLLGLFYIPQVYASSSRLSNKQKFS 182
 QY 180 LLRTPSADHVEAMVOLMLHFRWNWIIVLVSDTYGRDNGQLLGERVARRDICIATFOET 239
 Db 183 FLRTIPNDEHQATAMADIIEYFRWNWGTIAADDDYGRGIEKFPREAEERDICI DFSL 242
 QY 240 LPTIQPNQNTSEERQRLVTIIVDKLQOSTARVVVFPSPDLTYHFFNEVLNQFTGAVWI 299
 Db 243 I-----SQYSDSEIEQHVVEVI---QNSTAKVIVFSSGPDLEPLIKEIVRNITGTIWL 294


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QY 455 WDRSQNPQSVASYYPQLQKNIQDISWHTVNNTPMSMCKSRQSQGKKKPVGIHVC 514
Db 473 HIGGKYSYLKVGHW--AETLYLDVDSIHWS--RNSVPTSCSDPCAPNEMKNMQPGDVC 528
QY 515 FECIDCLPGTFLNHTDEYEQCAPNNEWSYQSTSCFKRQLVFLWHEAFTIAVALLAA 574
Db 529 WICIPCPEYEL--VDEFTCMDCGPGQWPTADLSGCYNLPEDYIRWEDAWAIGPVITAC 585
QY 575 LGFLSTLAILVIFWRHFQTPIVRSAGGPMCFMLTLLLVAYMVVVPVVGPKVSTCLCRQ 634
Db 586 LGFMCTCIVITVFKHNNTPLVKASGRELVCYLLFGVSLSCYMTFFFIAPKSPVICALRR 645
QY 635 ALPFLQTCICISCIASVFOIVCAF---KMASRPRAYSVMVRYQGVYVSMAFITVLKMV 691
Db 646 LGTGSTFAICYSALLTKTNCIARIFDGVKNGARPKFIS-----PSSQVFI-CLGLI 696
QY 692 IIVVIGMLATGL---SPTTR--TDPDDPKITIVSCNPNRNSLLFNSTSLDLSLVVGSFSA 746
Db 697 LVQIVMVSVWLLIETPGTRRYTLPEKRETVILKCNVK--DSSMLISLTYDVVVLILCTVYA 755
QY 747 YMGKELPTNNEAKFILTSMFTFTSSVSLCTFMSAYSGVLVITVILLV-TVLNLLAISL 805
Db 756 FKTRKCPENFEAKFIFTM---YTTCTIILAFILPFI---YVTSDDYRVQITTMCISSVL 809
QY 806 G-----YFGPKCYMILFVPERN 822
Db 810 SGFVVLGCLFAPKVVHILVFPQKN 833

RESULT 8
JH0562
metabotropic glutamate receptor 3 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: JH0562
R: Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A:Title: A family of metabotropic glutamate receptors.
A:Reference number: JH0561; MUID:92110002; PMID:1309649
A:Accession: JH0562
A:Molecule type: mRNA
A:Residues: 1-879 <TAN>
A:Cross-references: UNIPROT:P31422
A:Experimental source: brain
C:Comment: This protein is coupled to a G protein and evokes a variety of functions by
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-879/Product: metabotropic glutamate receptor 3 #status predicted <MET>
F:517-534/Domain: transmembrane #status predicted <TRI>
F:517-534/Domain: transmembrane #status predicted <TRI>
F:614-634/Domain: transmembrane #status predicted <TRI>
F:646-664/Domain: transmembrane #status predicted <TRI>
F:689-709/Domain: transmembrane #status predicted <TRV>
F:735-756/Domain: transmembrane #status predicted <TRV>
F:770-791/Domain: transmembrane #status predicted <TRV>
F:804-828/Domain: transmembrane #status predicted <VII>
F:209,292,414,439/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:1610,845/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 16.2%; Score 720.5; DB 2; Length 879;
Best Local Similarity 26.6%; Pred. No. 2.3e-46;
Matches 230; Conservative 145; Mismatches 353; Indels 137; Gaps 31;

QY 29 LPQDVLGLFSLHANMKGIHVLFLQVPMCKEYEVKIVGNLMQAMRPAVEINNDSSL 88
Db 35 IEGDVLVGLGFIPNKEKGTETECGRINDR-----GIQRLMALFPAIDKNDNVL 85
QY 89 LPQVLLGVEIVDVC-----YIGNNVQVLYFLAHEDN---LLP-----IQEDYSNYISRV 135
Db 86 LPQVLLGVEIVDVC-----YIGNNVQVLYFLAHEDN---LLP-----IQEDYSNYISRV 142
QY 136 VAVIGPDNSSESVMTVANFLSLFLPQITYSALSDRLKVRFPALLITTPSADHVEAMV 195

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Db 143 AGVIGSYSSVSTQVANLLRLFOIPQISVASTSAKLSDKSRDYFARTVPPDPFYQAKAMA 202
QY 196 QLMHLFRMNIIVLVSSDYGRDNGQLGERVARRDICIATFOETLPTLQPNQNTSBERQ 255
Db 203 EILRFNWTYVSVASBGDYGETIEAFQEARLNICIATAEKVGRSNIRKSVDS--- 258
QY 256 RLVTIYDKLQOSTARVVVVV---SPDLTYLHFNEVLQRNFTGAVMIASSEWALDPVLHN 312
Db 259 ---VIRELLQKPNARVVVVLPMRSDDSRELIAAANRV-NASFT---WVASDGMGAQESIVK 311
QY 313 LTELGHGLTGLTIGTISQVPI-----PGSFBERGWPQAGPEPLSRTS 354
Db 312 GSEHVAIGA-ITILELASHPVQRDRYFQSLNPNYNNHRNPMFRDWE----- 356
QY 355 QSTYCN-----QECNCLNATLSNTILSRGVRVSVYSVAVAAHALHSLG-- 404
Db 357 QKQCSLQNKRNHRQVCDKHLAIDSS-----NYEQESKIMFVNNAVYMAHALHMQRTL 411
QY 405 CDKST--CTKRVVYPMQLL--BEIKVNFVL-----LDHQIFFDQGDVALHLEIVQW 453
Db 412 CPNTTKLDCAMKILDGKLYKEYLLKINFAPFNPKGADSIKFDFTFGDMGRYNNFNL 471
QY 454 QWDSQNPQSVASYYPQLQKNIQDISWHTVNNTPMSMCKSRQSQGKKKPVGIHVC 513
Db 472 QQTGKYSYLKVGHW--AETLSLDVDSIHWS--RNSVPTSCSDPCAPNEMKNMQPGDVC 527
QY 514 CFECIDCLPGTFLNHTDEYEQCAPNNEWSYQSTSCFKRQLVFLWHEAFTIAVALLA 573
Db 528 CWICIPCPEYEL--VDEFTCMDCGPGQWPTADLSGCYNLPEDYIKWEDAWAIGPVITIA 584
QY 574 ALGFLSTLAILVIFWRHFQTPIVRSAGGPMCFMLTLLLVAYMVVVPVVGPKVSTCLCR 633
Db 585 CLGFLCTCIVITVFKHNNTPLVKASGRELVCYLLFGVSLSCYMTFFFIAPKSPVICALR 644
QY 634 QALPFLCTCICISCIASVRSQIVCAF---KMASRPRAYSVMVRYQGVYVSMAFITVLKM 690
Db 645 RLGLGSTFAICYSALLTKTNCIARIFDGVKNGARPKFIS-----PSSQVFI-CLGL 695
QY 691 VIVVIGMLATGL---SPTTR--TDPDDPKITIVSCNPNRNSLLFNSTSLDLSLVVGSF 745
Db 696 ILQIVMVSVWLLIETPGTRRYTLPEKRETVILKCNVK--DSSMLISLTYDVVVLILCTV 754
QY 746 AYMGKELPTNNEAKFILTSMFTFTSSVSLCTFMSAYSGVLVITVILLV-TVLNLLAIS 804
Db 755 AFKTRKCPENFEAKFIFTM---YTTCTIILAFILPFI---YVTSDDYRVQITTMCISSV 808
QY 805 LG-----YFGPKCYMILFVPERN 822
Db 809 LSGFVVLGCLFAPKVVHILVFPQKN 833

RESULT 9
JH0563
metabotropic glutamate receptor 4 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: JH0563; I58149
R: Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A:Title: A family of metabotropic glutamate receptors.
A:Reference number: JH0561; MUID:92110002; PMID:1309649
A:Accession: JH0563
A:Molecule type: mRNA
A:Residues: 1-912 <TAN>
A:Cross-references: UNIPROT:P31423
A:Experimental source: brain
R: O'Hara, P.J.; Sheppard, P.O.; Thøgersen, H.; Venezia, D.; Haldeman, B.A.; McGrane, V.
Neuron 11, 41-52, 1993
A:Title: The ligand-binding domain in metabotropic glutamate receptors is related to
A:Reference number: I58149; MUID:93332699; PMID:8338667
A:Accession: I58149
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

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A:Residues: 1-123,'R',125-912 <RES>
 A:Cross-references: GB:M90518; NID:G205400; PIDN:AAA93190.1; PID:G205401
 C:Comment: This protein is coupled to a G protein and evokes a variety of functions by m
 C:Genes: GLUR4
 C:Superfamily: metabotropic glutamate receptor 4
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
 F:1-32/Domain: signal sequence #status predicted <SIG>
 F:33-912/Product: metabotropic glutamate receptor 4 #status predicted <MET>
 F:588-610/Domain: transmembrane #status predicted <TRI>
 F:625-645/Domain: transmembrane #status predicted <TRI>
 F:657-675/Domain: transmembrane #status predicted <III>
 F:700-720/Domain: transmembrane #status predicted <III>
 F:751-772/Domain: transmembrane #status predicted <TRV>
 F:786-807/Domain: transmembrane #status predicted <TRV>
 F:822-847/Domain: transmembrane #status predicted <VII>
 F:98,301,454,484,569/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:621,689,695,859,870/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 16.1%; Score 714; DB 2; Length 912;
 Best Local Similarity 26.3%; Pred. No. 7.6e-46;
 Matches 239; Conservative 160; Mismatches 348; Indels 162; Gaps 36;

QY 8 ICSLELL--WV---LAEPAN---SDFYLPDGYLLGGLFSLHNMKGIVHLNFIQVPM 59
 DB 16 LCLLSLYAPWVPSSLGKPKGPHMNSIRIDGDTLGLFPVHGRGS-----EGKAC 67
 QY 60 KEYEVKIVGNLMQAMRFAVEEINDDSLPGVLLGYEIVDVYCNVNNVQPVLYFLAHD 119
 DB 68 GELK-KEGIHLEAMLFADLRINDPDLLPNTILGARILDTC--SRDTHALEQSITFVQ 124
 QY 120 NLLPIQEDYSNY-----ISRVAVIGPNSESVMTVANFLSLFLPQITYSAI 167
 DB 125 AL--IEKDGTEYRCGSGGPPITTKPERVGVIGAGSSVSIIVANILRLFKIPQISYAT 182
 QY 168 SDELKDKVRFPALLRTTPADHHVAVMQLMLHFRWNWIIIVSVSTYG-----216
 DB 183 APDLSDNSRDYDFSRVPVSDTYQAQAMVDIVALKMNVYSTLASEGSGVEAFIQKS 242
 QY 217 RINGQLLGERVARRDICIATQETPLTPQNQNTSEEROLATIVDKLOOSTARVVVPS 276
 DB 243 RENG-----GVCIAQSVKIPR-EPTGEFDKIIRL-----LETSNARGIIFPA 285
 QY 277 PDLTYLHFFNEVLRQNTFC-AVMIASESWAID--PVLHNLTELHGLTFLGITI--QSV 331
 DB 286 NEDDIRRVLEARRANQTHFFWMSGDSWGSAPVL-RLEVAE-----GAVTILPKMS 340
 QY 332 IGFSEFEFWGQAGPPPLSRT-----SQSYTCNQECNCLNATLSFTNLTIRLSG 381
 DB 341 VRGDFRYS-----SRLDNNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKKCTN 390
 QY 382 ERV-----VYSVYSVAVYAVAHLSLLCGDKSTCTKRV-----VYPWQLL 421
 DB 391 RERICQDSAYEGEKVQFVIDVAYANGHALHAM---HRDLCPGRVGLCPRPMDPVDGTQL 447
 QY 422 EBIWKVNET-LDHOIFDPQGDVALHLEIVQWDRSONPPQSVASYYP-LQROLKNIQ 479
 DB 448 KYIRNVNFGIAGNPVTNENGDAFGVDYIYQYLRNGSAEYKVGISWTDLHLIERMQ 507
 QY 480 DISWTVNTIPMSCKRQSGQKKKPVGHVCCPECIDCLPGTFLNHTEDVEYEQACP 539
 DB 508 ---WFGSGQQLPRISICSLPQCPGERKTKVKGMACCHCEPC---TGYQVQVDYRTCKTP 561
 QY 540 NNEWSYQSTSCFKQLVFLWEHAPTIAVALLAALGFLSTLAILVIFWRHPTQIVRSA 599
 DB 562 YDMRTEKNTSCQPIPIVKLEWDSFWAVLPLFLAVVGTAAITLVVVVTFVRYNDTPIVKA 621
 QY 600 GGFMCFLMLTLLVAVMVPVVPVGPVKSTCLCROALPFLCPTICISIAVRSFOIVCAF 659
 DB 622 GRELSVLLAGFLCYATTFLMIAEPDLGTCSLRIFLGLGMSISYAAALLTKNRIYRIF 681
 QY 660 KMASFPFRAYSVMVYQGYVSMATITVLMVIVVIGMLATGSLPTTRTDPDPPKITIV- 718

DB 682 EQGKRSVSA---PRFISPASOLA-ITFILISLQLLIGICWVFV-----DPHSVVD 728
 QY 719 -----SCNPNYNSLLFNTSLDL-LLSVVGFS-----PAYMCKELPTNNVEAKFIT 763
 DB 729 FQDQRTLDPRFARGVLKCDISLISLCLGLYMLMVTCTVYAIKTRGVPETNEAKPIG 788
 QY 764 LSWTFYSSVSLCWFMSAYSG-----VLVTIVDLLVTLNLLLAISLG-YFGPKCYMI 815
 DB 789 FTW---YTCIVWLAFIPFPFGTSQSADKLYIQTTTLTVSVLSASVSLGMLNPKVYII 845
 QY 816 LFYPERNTP 824
 DB 846 LFHPEQNVP 854

RESULT 10
 JH0561
 Metabotropic glutamate receptor 2 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C:Accession: JH0561
 R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
 Neuron 8, 169-179, 1992
 A:Title: A family of metabotropic glutamate receptors.
 A:Reference number: JH0561; MUID:92110002; PMID:1309649
 A:Accession: JH0561
 A:Molecule type: mRNA
 A:Residues: 1-872 <TAN>
 A:Cross-references: UNIPROT:P31421
 A:Experimental source: brain
 C:Comment: This protein is coupled to a G protein and evokes a variety of functions by m
 C:Superfamily: metabotropic glutamate receptor 4
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
 F:19-872/Product: metabotropic glutamate receptor 2 #status predicted <SIG>
 F:19-872/Domain: signal sequence #status predicted <TRI>
 F:568-590/Domain: transmembrane #status predicted <TRI>
 F:605-625/Domain: transmembrane #status predicted <TRI>
 F:637-655/Domain: transmembrane #status predicted <III>
 F:680-700/Domain: transmembrane #status predicted <III>
 F:726-747/Domain: transmembrane #status predicted <TRV>
 F:761-782/Domain: transmembrane #status predicted <TRV>
 F:795-819/Domain: transmembrane #status predicted <VII>
 F:203,286,338,402,547/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:601,675,827,837,843/Binding site: phosphate (Ser) (covalent) #status predicted
 F:832/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 15.7%; Score 699; DB 2; Length 872;
 Best Local Similarity 26.9%; Pred. No. 9.9e-45;
 Matches 235; Conservative 154; Mismatches 368; Indels 116; Gaps 33;

QY 14 LLW-VLAEPAENSDYLPDGYLLGGLFSLH-----ANMKGIHNLFLQVPMCKEYEVKI 67
 DB 12 LLWGAVAEPAENKVKVLTLEGDLVLGLFPVHKGPAEECPVN-----EHR-----57
 QY 68 GYNLMQAMRFAVEEINDDSLPGVLLGYEIVDVYCNVNN-VOPVLYFLAHE-----DNL 121
 DB 58 GIORLEAMLFALDRINRDPHLLPGVRLGAHLSDCKTHALEQALDFVRLASLGADGS 117
 QY 122 LPIQED-----YSNYISRVAVIGPNSESVMTVANFLSLFLPQITYSAISDELRLKVR 176
 DB 118 RHICPDGYSYATHSDAPTAVTGVIGSYSDVSIQVANLLRLFOIPQISVASTSAKLSKSR 177
 QY 177 FPALLRTTPSADHHVAVMQLMLHFRWNWIIIVSVSDTYGRDNGQLLGERVARRDICIATF 236
 DB 178 YDFARTVPPDFPOKAMAEILRFNFTVYSTVASEGYGETGIEAFELARARNICVAT 237
 QY 237 QETLPTLPQNQNTSEEROLATIVDKLOOSTARVVVVF--SPDLTYLHFFNEVLRQNT 294
 DB 238 SEKV-----GRAMSRAAFEGVVRAL--LQKESARVAVLTFSDEARELLAATQRLNASFT 290
 QY 295 GAVMIASESW-AIDPVLHNLTELHGLTFLGITIQSVPFGFSBFRE-----WGQAGGPPP 349
 DB 291 ---WVASDGWGALESVVAG--SERAAEGA-ITIELASYPISDFASYFQSLDPPNNSRNPF 345

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Qy 350 LSRSTQSYTCNQECNCLNATLNTILSLGRVYVSVYAVVAHALHSL--LGCDK 407
Db 346 REFWEERFHCISFRQDCAAHSL---RAVPFEQBSKIMFVNAVYAMAHALHNRALCPN 402
Qy 408 ST--C--TKRVVYPMQLLEE-IWKYNFTL-----LDHQIFPDPOGDVALHLEIVQW--QWD 456
Db 403 TTHLCDAMRPVNGRRLYKDFVLNVKFDAPFRPADTDDEVFRDFDGDGIGRYNIPTYLRA 462
Qy 457 RSNPPFQSVASYYPQLQKLNQIDISWHTN-NTIPMSMCKRQSQKPKPGVGHVCCP 515
Db 463 SGRYRYQKVG--YWAEGLTLDTSFIPWASPSAGELPASRCSBPCLONEVKSVPQGEVCCW 520
Qy 516 ECIDCLPGTFLNHDEVEQACPNNEWSQSETSCFKQLVFLFLEHEAPTIAVALLAAL 575
Db 521 LCIPQCP--YEVLDFTACDGLGYWPNASLTGCELPQEVYRWGDMAVGPVTIACL 577
Qy 576 GFJSTLAILVIFWRHFQTPIVRSAGGPMCFMLTLVAVMVVYVYVGGPKVSPCLCROA 635
Db 578 GALATFLVGVFVRHNAFVVKASGRELCYLLGGVFLCYMTFVFIKTPSTAVCTLRRL 637
Qy 636 LFLPLCFITCICIAVRFOIVCAFPMASRPFRAYSVWRYQGPVYVMAFIVL---KMWI 692
Db 638 GLGTAFSVCSYALLTKTNRIARIFGGA---REGAQRPRFTSPASQVAICLALISGQLLI 693
Qy 693 VVIGMLATGLSPTRTPDPPDKITIVSCNPNYRN-SLENTSLDLLSVVGFSPAYMGKE 751
Db 694 VAAMLVVEAPGTGETAPERREVTLRC--NHRDASMLGSLAYNVLLIALCTLYAFKTRK 751
Qy 752 LPTNNEAKFTLSM-----TFYFTSS-----VSLCTFMSAYSGVLVITVDL 793
Db 752 CPENFNEAKFTGFTWYTCIIWLAFPIFYVTSDDYRVQVTTMCVSVLSGSV----- 804
Qy 794 LVTVLNLLAISLGVFGPKCYMILFYPERNTPAY 826
Db 805 ---VLGCL-----FAPKLHILFPQKQNVVSH 828

RESULT 11
A42916
metabotropic glutamate receptor mGluR5 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42916
R;Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
J. Biol. Chem. 267, 13361-13368, 1992
A;Title: Molecular characterization of a novel metabotropic glutamate receptor mGluR5 c
A;Reference number: A42916; MUID:92317054; PMID:1320017
A;Accession: A42916
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1171 <ABE>
A;Cross-references: UNIPROT:P31424; GB:D10891; NID:g220813; PIDN:BA001711.1; PID:d100218
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIN:107749, NCBI:P:107750)
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 15.4%; Score 682.5; DB 2; Length 1171;
Best Local Similarity 25.5%; Pred. No. 2.6e-43;
Matches 226; Conservative 153; Mismatches 344; Indels 165; Gaps 31;

Qy 28 YLPGDYLGGLFSLHANMKGIVHLNFLQVPMCKEYEVK-----IGYNLMQAMRFAYVEE 81
Db 30 HMPGDIIIGALFSVH-----H-----QPTVDKVKHRCGAVREYQVGIQRVEAMLHTLER 78
Qy 82 INNUSSLLPGVLLGVEIYDVVCYIS-----NNVQPVLYFLAHEDNLLPQEDSYNYS 133
Db 79 INSDPTLLPNTIGCEIRDCSWHSAVALEQSIETFIKRLSLISEEGLVRCVGDGSSSPRS 138
Qy 134 R--VVAVIGPNDSVMTVNVANFLSLFLPLQITYSAISBELRDKVRFAPALLKTPSGADHV 191
Db 139 KKPVGIVGPGSSVAIVQNLQLLQFNIPQIAYSATSMDSLDKTLFKYFMRVVPDSDAQA 198
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Qy 192 EAMVOLMLHFRWNMIIVLVSSDITYGRDNGQLLGERVARRDICIAFQTLPTLPQNNQWTS 251
Db 199 RAMVDIVKRYNWTIVSAVHTEGNYGESMEAFKXMSAKEGICIAHSYKI-----YSN 250
Qy 252 EERQRLVTVIDKLQ--STARVWVVSFDTLTHFFNEVLNQFTGA-VWIASSEWALDP 308
Db 251 AGEQSDFKLKCLSLRSHLPKARVVVACFCEGTVVRLGLMAMRRRLAGLFFLLGSDGWA--- 307
Qy 309 VLHNLTLGLHGTFLGITI--QSVPI-----PGSESEFEWEPQAGPP 348
Db 308 DRVDVTDGYQREAVGGITIKLQSPDVKNFDDYVILKLPETNLNRPWFQEFQWHRFQCRLE 367
Qy 349 PLRSTQSYTCNQECNCLNATLNTILSLGRVYVSVYAVVAHALHSLG 404
Db 368 GFAQENSKY--NKTC-----NSSLTLRTHHVQDSKMGVFINAIYSMAYGLHN-- 413
Qy 405 CDKSTC-----TKRVVYPMQLLEE-IWKYNFTL-LLDHOFDPDQGDVALHLEIVQW-- 454
Db 414 -QMSLCPGYAGLCDAMKPIDGRKLLDSLMKTNFTGVSGDMILLFDENGDSFGRYIMNFK 472
Qy 455 -----WDRSQNPQSVASYYPQLQKLNQIDISWHTVNTNTPMSMCKRQSQ 501
Db 473 MGKDYFDYINVGWDNG-----ELKMDDDDEVMSKKNII-RSVCSECEK 516
Qy 502 GQ-----KKXPGVIHVCFCIDCLPGTFLNHTEDVEYEQACPNNEWSQSETSCFKQLV 557
Db 517 GQIKVIRKGEVS---CCWTCCTCKNEVY---FDEYTCACQLGSMWPTDLDLTCGDLIPVQ 570
Qy 558 FLEWHEAPTIAVALLAALGELSTLAILVIFWRHFQTPIVRSAGGPMCFMLTLVAVMV 617
Db 571 YLRMGDPEPIAAVVVACLGGLLTLFVTFIYIRDTVPWKSSESLCYIILAGCLGVL 630
Qy 618 VPVYVGGPKYSTCLCRQALPCLCTICISCIATVRSFOIVCAF-----KMASRFPFRAYS 672
Db 631 TFLIAPKQIYCYLQIGIGLSFAMYSALVTNTNRIARLAGSKKCICTKKPRFMSAC 690
Qy 673 VRYQGPVYVMAFIVLVKVIIVIGMLATGLSPTRTPDPPDKITIVSCNPNYRN-SLLFN 731
Db 691 AQ-----LVIAFILICIQLGIIIVLFT-----MBPPD-----IMHDYPSIREVYL 733
Qy 732 TSLDLLLSVVGFSS-----FAYMGKELPTVNEAKFTLSMTFVTSVSLCTFMSA 782
Db 734 TTNLGVVTPGYNGLLILSLCTFYAFKTRNVPANNEAKYIAFTM---YTTICIIWLAFVPI 790
Qy 783 YSGVLVTVIDLLVTVLNLALISLG-YFGPKCYMILFYPERNTPAYFNS 829
Db 791 YFGSNYKIITWCFSVLSATVALGCMFVPKVYIILAKPERNVRSFAFT 838

RESULT 12
JC2132
metabotropic glutamate receptor 5 A - human
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
C;Accession: JC2132
R;Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
A;Title: Molecular cloning and the functional expression of two isoforms of human metab
A;Reference number: JC2131, MUID:94197696; PMID:7908515
A;Accession: JC2132
A;Molecule type: mRNA
A;Residues: 1-1180 <MIN>
C;Comment: This protein is coupled to guanine nucleotide binding proteins.
C;Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein
F;580-604/Domain: transmembrane #status predicted <TM1>
F;617-637/Domain: transmembrane #status predicted <TM2>
F;644-664/Domain: transmembrane #status predicted <TM3>
F;694-714/Domain: transmembrane #status predicted <TM4>
F;738-759/Domain: transmembrane #status predicted <TM5>
F;773-794/Domain: transmembrane #status predicted <TM6>
F;803-827/Domain: transmembrane #status predicted <TM7>

Query Match 15.1%; Score 673; DB 2; Length 1180;
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	Matches	227;	Conservative 154;	Mismatches 336;
			Indels	178;
			Gaps	33;
QY	28	YLPDGIILGGLFSLHANMKGIVHLNFIQLQPMCKEYEVKV-----H-----OptVDVKHERKCGAVRQYGIQRVEMLHTLER	81	
Db	30	HMPGDIIIGALFSVH-----H-----OptVDVKHERKCGAVRQYGIQRVEMLHTLER	78	
QY	82	INNDSSLLPGVLLGYEIVDVCYISN-NVQPVLYFLAHEDNLLPQED-----YSN	130	
Db	79	INSDPTLLPNITLCEIRDCSWHSAVALEQSIIEFI--RDSLISEEGLVRCVCDGSSSS	136	
QY	131	YISR--VVAVIGPNSSEVMVNFSLFLLPQITYSAISDELKDKVRFPPALLRTTSPAD	188	
Db	137	FRSKPIVGIWGPGSSVAIQVNLQLFNIPQIAYATSMDLSDKTLFKYFMRVPSDA	196	
QY	189	HHVEAMVOLMLHFHFNWNIIVLVSDTYGRDNGQLLGERVARRDICIAFQETLPTLQPNQN	248	
Db	197	QQARAMVDIVKRYNNTVSAVHTEGNYGESGMEAFKQMSAKEGICIAHSYKIYSNAGEQS	256	
QY	249	MTSEERQLVTIYDVKLOOS-----TARVVVVFSPDLTLHYHFFNEVLRQNTFGA-VMIAS	301	
Db	257	F-----DKLKUKITSHLPKARVACFCBGMTVRGLLAMRRLGLAGFELLGLGS	304	
QY	302	ESWAIDPVLNLTGLHGLTGLGITI--QSVPI-----PGSEPREW	341	
Db	305	DGWA--DRYDVTDGYQREAVGGITIKLOSPDVKWFDDYILKLPETHRNPWFQEWQH	361	
QY	342	GPOAGPPPLGRTSGSYTCNGECNCLNATISFNTILRSGERVVYS---VYSAYVAH	397	
Db	362	RFQCRLEGFPQENSKY--NKTC-----NSSLTALKTHHVQDSKMGFVINAISWAY	409	
QY	398	ALHSLLGCDKSTC-----TKRVVYPWQLLEIWKVNETI-LLDHOIFPDPOGDVALHL	448	
Db	410	GLHNW---QMSLCPGYAGLCDAMKPIDGRKLLSLMTNFTFVSGDITLFDENGDSGRY	466	
QY	449	EIVQWQ-----WDRSQNPQSVASYIPLQRLKNTQDISWHTVNNNTIPMSM	494	
Db	467	EIMNFEMGKDYFYINVGSWDNG-----ELMKDDDEWSSKSNII-RSV	510	
QY	495	CSKRCQSQQ---KKKPVGIHVCCFICIDCLPGTFLNHTEDYEICQACPNNWSYQSETS	550	
Db	511	CSPECKEKGQIKVIRKGEVS--CWCTCTPKENEYV--FDEYTCRACQLGSWPTDGLTG	564	
QY	551	CFKRQLVFLSEWHEAPTAVALLAALGFLSTLAILVIEWRHQTPIVRSAGSECMFLMLTL	610	
Db	565	CDLIPQVYLRWGDEPEIAAVVFACLGLLATLFTVTVFIIYRDTPVUKSSRELCTYIILAG	624	
QY	611	LLVAYMVVYVYGGPKVSTCLCQALPFLCFTICICIAVRSFOIVCAF-----KMASRF	665	
Db	625	ICGLYLCTFCILAKPKQIYCVLQIRIGIGLSPAMSYSALVTKTNRARIILAGSKKKICTKK	684	
QY	666	PRAYSIVRYQGPVVSMAFITLWKWIVVICMLATGLSPITRTDPPDKTIIIVSCNNYR	725	
Db	685	PRFMSACQ-----LVIAFILICIQLGIIIVALFI-----MEPPD-----IMHDPYSIR	727	
QY	726	N-SILLENTSLLLLSVVVGFS-----PAYMGKELPTNYNEAKFITLSMTFYFTSSVS	775	
Db	728	EVYLICNTTNLGVVTPLYNGLLLSCTFYAFKTRNVPANFEAKYIAFTM---YITCII	784	
QY	776	LCTFMSAYSGLVITIVDILLVTIVNLNLAISIG-YFGPKCYMILFPERNTPAYFNS	829	
Db	785	WLAFVPIYFGSNYKIITMCFBSVLSAFVALGCMFVPRKVIYIILAKPENRVSFAFTI	839	

RESULT 13
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metabotropic glutamate receptor 5 B - human
C:Species: Homo sapiens (man)
C:date: 28-Aug-1995 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
C:Accession: JC2131
R;Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
A:Title: Molecular cloning and the functional expression of two isoforms of human metabo

A:Reference number: JC2131; MUID:94197696; PMID:7908515	
A:Accession: JC2131	
A:Molecule type: mRNA	
C:Residues: 1-1212 <MNU>	
C:Comment: This protein is coupled to guanine nucleotide binding proteins.	
C:Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein	
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F:644-664/Domain: transmembrane #status predicted <TM3>	F:694-714/Domain: transmembrane #status predicted <TM4>
F:738-759/Domain: transmembrane #status predicted <TM5>	F:773-794/Domain: transmembrane #status predicted <TM6>
F:803-824/Domain: transmembrane #status predicted <TM7>	
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Best Local Similarity	25.4%; Pred. No. 1.4e-42;
Matches 227; Conservative 154; Mismatches 336; Indels 178; Gaps 33;	
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DB 30 HMPGDIIIGALFSVH-----H-----QPTVDKVERKCGAVRQYGIQRVEAMLHTLER 78	
QY 82 INNDSSLLPGVLLGYEIVDVCYISN-NVQPVLYIPLAHEDNLLPQED-----YSN 130	
DB 79 INSDPTLLPNITLCETRDSCWHSAVALEQSIIEFI--RDSLISSEEEGLVRCVDGSSS 136	
QY 131 YISR--VVAVIGPDSSEVMVFANFLSILFLLPQITYSAISDELKDKVRFAPALLRTTSPAD 188	
DB 137 FRSKPIVGLPGSSSSVAIQVMLLQFLNIPQIAYSATSMDLSDKTLFKYFMRVFPEDA 196	
QY 189 HHVEAMVQLMLHFRNMNIIIVLSSDITYGRDNGQLLGERVARRDICIAFQETLPTLPQNQN 248	
DB 197 QQARAVMDIVKRYNWTVSAVHTGNYGESGMEAFKDSAKEGICIAHSYKIYNSAGEQS 256	
QY 249 MTSEERQLVTIVDKLOS-----TARVVVFPSPDLTLVHFNEVLKQNETGA-VMIAS 301	
DB 257 F-----DKLLKKTUSHPKARVAVACFCEGNTVTRGLLMMARLGLAGEFLILGS 304	
QY 302 ESWAIDPVLHNLTLBGLHGLFLGITI--QSVPI-----PGSEFREW 341	
DB 305 DGWA---DRDVTVDGYOREAVGGITIKLQSPDVKWFDDYVILKLPETHNRHPWFQEFWQH 361	
QY 342 GPQAGPPLSRTSQTNCQECNCLNATLSFNTILRLSGERVVYS---VYSAYVAH 397	
DB 362 RFQCRLEGFPQENSKY--NKTC-----NSSLTLKTHHVQDSKMGFVINALIYSMAY 409	
QY 398 ALHSLLCDSKTC-----TKRVVYPVWOLLEIKWKNFT-LLDHQIFDPDQGDVALHL 448	
DB 410 GLHNM---QMSLCPGYAGLCDAMKPIDGRKLLESIMKTNFTGVSGDITLFDENGDSFGRY 466	
QY 449 EIVQWQ-----WDRSQNFQSVASYPLQRLKNIQDISWHTVNNITPMSM 494	
DB 467 EIMNFKMGKDYFDYINVGWDNG-----ELKMDDEVKSKSNII--RSV 510	
QY 495 CSKRCQSQG---KKKPVGHVHCCECIDCLPGTFLNHTDEYECQACPNNMSYQSETS 550	
DB 511 CSEPCXGQIKVIRKGBVS--CWTCTCPKENEYV--FDEYTKACQLGSMPTDLDLTG 564	
QY 551 CFKRQLVFLWEHAPTAVALLAALGPLSTIALIIVFWRHFQPTPIVRASAGGPMCFMLTL 610	
DB 565 CDLIPVQYLRMGDPEPIAAVFAVLGLATLFTVTVWFPIIYRDTTPVVKSSRELICYIILAG 624	
QY 611 LLVAYMVVVPVGPVKYSTCLCRQALPFLCFTICISCIASVRSQIVCAF-----KMASRF 665	
DB 625 ICGYLCTCFLIAKPKQIYCYLQIRIGISLSPMSYSALVTKTRIAKILAGSKKCICTKK 684	
QY 666 PRAYSIVWRYQGYPVSMAFITVLKMWIVTIGMLATGLSPTRTRDPDPDKITIVSCNPYR 725	
DB 685 PRFMSACAQ-----LVIAFLICIQLGIIIVAFI-----NEPPD----IMHDYPSIR 727	
QY 726 N-SLLFNWTSJDLILLSVVVGFs-----FAYMGKBLPTNYNBAKFTILSMYFTFTSSVS 775	
DB 728 EVLICTNLTNGVVTPLGYNGLLIISCTCFYAFKTRNVNPNANAKYIAFTM---YITCII 784	

QY 776 LCTFMSAYSGVLTIVDVLVTLNLLAISLG-YFGPKCYMILFYPERNTPAYFNS 829
 Db 785 WLAFVPIYFGSNKYIITWCFSVLSATVAGCMFVPKVYIILAKPVRNSAFT 839

RESULT 14
 A46742
 metabotropic glutamate receptor, mGluR6 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: A46742
 R:Nakajima, Y.; Iwakabe, H.; Akazawa, C.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi
 J. Biol. Chem. 268, 11868-11873, 1993
 A:Title: Molecular characterization of a novel retinal metabotropic glutamate receptor m
 A:Reference number: A46742; MUID:93280152; PMID:8389366
 A:Accession: A46742
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-871 <NAK>
 A:Cross-references: UNIPROT:P35349; GB:D13963; NID:g391856; PIDN:BA03066.1; PID:g391857
 A:Experimental source: retina
 A>Note: sequence extracted from NCBI backbone (NCBIN:133246, NCBI:P:133250)
 C:Superfamily: metabotropic glutamate receptor 4
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 15.0%; Score 668.5; DB 2; Length 871;
 Best Local Similarity 26.6%; Pred. No. 2e-42; Indels 133; Gaps 34;
 Matches 241; Conservative 151; Mismatches 380

QY 11 LFLLWLVAE---PAENSDFYLPDGLLGGFLSHANMKGIHFLNLFQVPMCKEYEVKVI 67
 Db 8 LLWLAWLSQAGIACGAGSVRLAGGLTGLGFPVHARGAACGACGALK-----KEQ 58

QY 68 GYNLMQAMRFAVEEINNDSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHENLPIQED 127
 Db 59 GVRLEAMLYALDRVADPELLPGVRLGARLLDTC--SRDTYALEQALSFQALIRGRD 116

QY 128 -----YSNVISRVAVIGPDNSSEMTVANFSLFLPLQITYSALSDLR 172
 Db 117 GDEASVRCGGVPLRSAPPERRVAVVGASASSVIMVANVLRFAIPQISTASAPELS 176

QY 173 DKVRFPALLRTPSADHVEAMVQLMHRFNWIIIVLSSDYGNDQQLGERVAR-- 230
 Db 177 DSTRYDFPSRVVPPDSYQAMVDIVRALGNVYSTLASSENYG-ESGVEAFVQISREAG 235

QY 231 DICTAFQETLTPQNOMTSEERQRLVTVDKLQOSTARVVVPPSDLTLYHFNFVLR 290
 Db 236 GVCIAQSIKIPR-BPKGFEHFKVIRL-----METPNARGIIIPANEDDIRRVLEATRQ 288

QY 291 QNFTG-AWIASSEWA--IDPVLHNLTE--LGHGTFLGITI--QSVPIPGFSREWGP 343
 Db 289 ANLTGHFLWVGSDSWGSKISPL-NLEBAVG-----AITLPKRAIDGFDQYF---- 337

QY 344 QAGPPPLSRTSQSYTCN-----QECNDC--LNATLSFNITLRSGER----- 383
 Db 338 -----WTRSLNNRRNIWFAEFWEENFNCKLTSSGGQSDSTRCTGEERIGQDSAYEQ 391

QY 394 --VTVSVYSAVAVAHLSL--LGCDSXSTKRVVYVWQ---LLEETWKNFT--LLDHQ 435
 Db 392 EGRQVQFVDAVYATAHALSHKHQALCPGHTGLCPAMEPTDGRLLHYTRAVRFGNSAGTP 451

QY 436 IFFPDQGVVALHLEIVQWQ---WDRSQNPFQSVASYVPLQRLKNIQDISWHVNTNTPM 492
 Db 452 VMFNENGDAPEGYDIFQYQATNGSSAGGYQAVGQWAEALR--LDMEVLRWSDGHEVPP 509

QY 493 SWCKRCQSGQKKPVGVHVCCEICDCLPGTFLNHTDEVEYECQCPNNEYSQETSFCF 552
 Db 510 SQCSLPCGPGERKKNVGVPCWCHCEACDGYRF---QVDEFTCEACPGDMRPTNHTGCR 566

QY 553 KQQLVLEWHEAPTIATVALLAALGFLSTLAILVIFWRHFQPTIVRSAGGPMCFMLTL 612
 Db 567 PTFVRLTWSSPWAALPULLAVIGIMATTIMATFMRNDPTIVRSAGRELSYLLTGIF 626

QY 613 VAYMVVYVYVGPVKVSTCLCQALFPLCFCTICISIAVRSPQIVCAFPMASRFPRAYSW 672
 Db 627 LIVAITFLVAEPCAAIACARRLLGLGTLTYSALLTKNRIYRIFEOGKRSTV----- 681

QY 673 VRYGQPVY---SMAFITVLMKVIIVIGMLA-TGLSP-----TTTTP-DPDDPKIIVS 719
 Db 682 ---PPPFISPTSQLVITFGLTSLQVGVIAWLAGQPPHSDVYBEQRTVDPEQAR-GVLK 737

QY 720 CNPNYRNSLLFNLSLDLLSVGFSFAYMCKEPTNNYNEAKFILTSTFTFTSVSLCTF 779
 Db 738 CDMW-DLSLIGCGYSLLMVTCVYAIKARGVPETNEAKPIGFTM---TTTCLIIWAF 793

QY 780 MSAYSG-----VLVTIVDVLVTLNLLAISLG-YFGPKCYMILFYPERNTPAYFNSMI 831
 Db 794 VPFFGTGAQAEKIIYITTTTLTVSLSSASVSLGMLVYPKTYVILFHPQNVQKRSLK 853

QY 832 QGYTM 836
 Db 854 KTSTM 858

RESULT 15
 I49142
 metabotropic glutamate receptor 8 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: I49142
 R:Duvoisin, R.M.; Zhang, C.; Ramonell, K.
 J. Neurosci. 15, 3075-3083, 1995
 A:Title: A novel metabotropic glutamate receptor expressed in the retina and olfactory
 A:Reference number: I49142; MUID:95239344; PMID:7722646
 A:Accession: I49142
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-908 <RES>
 A:Cross-references: UNIPROT:P47743; EMBL:U17252; NID:g854728; PIDN:AAA68149.1; PID:g854
 C:Genetics:
 A:Gene: mGluR8
 C:Superfamily: metabotropic glutamate receptor 4
 C:Keywords: neurotransmitter receptor

Query Match 15.0%; Score 668.5; DB 2; Length 908;
 Best Local Similarity 25.2%; Pred. No. 2.1e-42;
 Matches 232; Conservative 174; Mismatches 368; Indels 147; Gaps 39;

QY 4 RAKTICSLFFLL-----WVLA--EPAENSDF-----YLPDGLLGLGFLSLHA-NMKGIIVHL 51
 Db 6 KRSTSCPCFFLLTAKFYMLTMMQTHSQBYAHSIIRLDGDIILGLFPVHARGKGV--- 62

QY 52 NFLQVPMCKEYEVKVIYGNLMQAMRFAVEEINNDSLLPGVLLGYEIVDVCYISNNVQPV 111
 Db 53 -----PCGDLK-KEKGHRLAEMLYAIDQTNKPDLLSNITLGRILDTG--SRDTVAL 113

QY 112 LYFLAHENLPIQEDYSNY-----ISRVAVIGPDNSSEMTVANFSLFL 159
 Db 114 EQSLTFVQAL--IEKSDASDVKCAANGDPPIFTKPKISGVIGAAAASSVIMVANILRLPKI 171

QY 160 POITYSALSDLRDKVRFPALLRTPSADHVEAMVQLMHRFNWIIIVLSSDYGNDQQLGER 219
 Db 172 POISYASTAPELSNTRYDFRSVVPPDSYQAMVDIVRALGNVYSTLASSENYG-ES 230

QY 220 QQLLGERVAR--DICTAFQETLTPQNOMTSEERQRLVTVDKLQOSTARVVVVFSP 277
 Db 231 GVEAFTQISREIGGVCIQAQSKIPR-BRPCEFEKIKRL-----LETNARAVIMEAN 283

QY 278 DLTLYHFNFVLRQNFUG-AWIASSEWA--IDPVLHNLTELHGLTFLGITI--QSVPI 332
 Db 284 EDDIRGILEAAKLNQSGHFLWIGSDSWGSKIAFV-YQOEIEAE---GAVTILPKRASI 338

QY 333 PG-----ESEPRE--WGQAPGPPPLSRTSQSYTCNQCDCNCLNATLS 372
 Db 339 GFDRIYFRSRFLANNRRNVWFAEFSEGNFGCKSGSHG-KRNSHIKCT-----G 386

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 2, 2004, 09:16:39 ; Search time 1068 Seconds
(without alignments)
17512.816 Million cell updates/sec

Title: US-10-035-045-20

Perfect score: 3563

Sequence: 1 agcctggcagtgccctcagg.....tggacacccctgtgaccatc 3563

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3563	100.0	3563	5 AAD17517	Aad17517 Human tas
2	3563	100.0	3563	6 AEN84919	Abn84919 Human tas
3	3403.8	95.5	8001	6 AAL38463	Aal38463 Genomic D
4	3403.8	95.5	8001	9 ACA62667	ACA62667 DNA encod
5	3398.6	95.4	4256	10 ADC86148	Adc86148 Human GPC
6	3398.2	86.7	3200	10 ADK90723	Adk90723 Human tas
7	2965.4	83.2	3115	8 AB242555	Abx42555 Human G p
8	2687	75.4	2687	5 AAD17508	Aad17508 Human tas
9	2157.4	60.6	2685	12 ADI40945	Adi40945 Human G p
10	2099.2	58.9	3489	4 AAS14574	Aas14574 Human cdn
11	2099.2	58.9	3489	12 ADG19751	Adg19751 Human G p
12	2086.2	58.6	3446	10 ADJ93108	Adj93108 Human G-C
13	2080.4	58.4	3458	6 AAL38462	Aal38462 cDNA enco
14	2080.4	58.4	3458	9 ACA62666	ACA62666 cDNA enco
15	2080	58.4	2729	6 ABL55952	Ab155952 Human G-p
16	2079.8	58.4	2727	8 ABS57070	Ab57070 Human DNA
17	1961.4	55.0	2592	12 ADI40941	Adi40941 Human G p
18	1917	53.8	2579	10 ADC26322	Adc26322 Human NOV
19	1897	53.2	2559	6 AEN84920	Abn84920 Human tas
20	1897	53.2	2559	8 ABZ68280	Abz68280 Nucleotid
21	1897	53.2	2559	10 ADK90724	Adk90724 Human tas

22	1897	53.2	2559	12 ADG73583	Adg73583 Human TIR
23	1895.4	53.2	2559	6 ABK47345	Abk47345 cDNA sequ
24	1893.8	53.2	2559	6 AAS97395	Aas97395 Human SAC
25	1893.8	53.2	2559	12 ADG19753	Adg19753 G protein
26	1893.8	53.2	2559	12 ADM15734	Adm15734 Human SAC
27	1885	52.9	2553	5 AAD17509	Aad17509 Human tas
28	1885	52.9	2553	10 ADK90738	Adk90738 Human tas
29	1883.4	52.9	2553	10 ACC69594	Acc69594 Human swe
30	1869.4	52.5	2739	6 ABK16615	Abk16615 Human G-C
31	1787.6	50.2	2415	10 ADC12739	Adc12739 Human GPC
32	1747.4	49.0	2490	12 ADI40943	Adi40943 Human G p
33	1673.2	47.0	2460	12 ADL70548	Adl70548 Human G-p
34	1612.4	45.3	2421	6 AAL50394	Aal50394 Human gen
35	1312.8	36.8	11809	6 AAS97394	Aas97394 Murine SA
36	1312.8	36.8	11809	12 ADM15732	Adm15732 Murine SA
37	1293	36.3	3240	10 ADK90726	Adk90726 Mouse tas
38	1291	36.2	3200	10 ADK90731	Adk90731 Mouse tas
39	1190	33.4	1788	6 AAD34459	Aad34459 Human GPC
40	1086	30.5	1086	6 AAS98148	Aas98148 Human DNA
41	977	27.4	1113	6 AAD34458	Aad34458 Human GPC
42	876	24.6	876	5 AAD17507	Aad17507 Human tas
43	835.6	23.5	2577	5 AAD17514	Ad17514 Rat taste
44	835.6	23.5	2577	6 AEN84925	Abn84925 Rat taste
45	835.6	23.5	2577	8 ABZ68277	Abz68277 Nucleotid

ALIGNMENTS

RESULT 1

AAD17517

ID AAD17517 standard; DNA; 3563 BP.

XX AAD17517;

XX 10-DEC-2001 (first entry)

XX Human taste receptor, hTlR3 full-length genomic DNA.

XX Human; taste-cell-specific G protein-coupled receptor; TlR3; drug; genetic modulation; pharmaceutical; taste sensation; food industry; chemosensory transduction; chromosome 1p36.2-1p36.33; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..3381
FT /product= "Human taste receptor, hTlR3 protein"
FT /tag= a
FT intron 1..210
FT /tag= b
FT /number= 1
FT /cons_splice= (5'site:NO, 3'site:NO)
FT exon 211..401
FT /tag= c
FT /number= 1
FT intron 402..502
FT /tag= d
FT /number= 2
FT exon 503..802
FT /tag= e
FT /number= 2
FT intron 803..945
FT /tag= f
FT exon 946..1723
FT /tag= g
FT /number= 3
FT intron 1724..1837
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FT /number= 4
FT exon 1838..2041
FT /tag= i

FT intron /number= 4
 FT 2042..2175
 FT /*tag= j
 FT /number= 5
 FT 2176..2296
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 FT /number= 5
 FT intron 2297..2422
 FT /*tag= l
 FT /number= 6
 FT 2423..3381
 FT /*tag= m
 FT /number= 6
 FT intron 3382..3563
 FT /*tag= n
 FT /number= 7
 FT /cons_splice= (5'site:NO, 3'site:NO)
 XX W020016563-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 07-MAR-2001; 2001WO-US007265.
 XX
 XX 07-MAR-2000; 2000US-0187546P.
 PR 07-APR-2000; 2000US-0195536P.
 PR 06-JUN-2000; 2000US-0209840P.
 PR 23-JUN-2000; 2000US-0214213P.
 PR 17-AUG-2000; 2000US-0226448P.
 PR 03-JAN-2001; 2001US-0259227P.
 XX
 PA (SENO-) SENOMYX INC.
 XX
 XX Adler JE, Zozulya S, O'connell SM, Li X, Staszewski L;
 PI WPI; 2001-582267/65.
 DR P-PSDB; AA010366.
 XX
 XX New mammalian taste-cell-specific G protein-coupled receptor polypeptides
 PT for identifying compounds that modulate taste signaling are useful in
 PT food, to modulate the sweet taste of foods or drugs.
 XX
 PS Claim 1; Page 71-72; 119pp; English.
 XX
 CC The invention relates to mammalian taste-cell-specific G protein-coupled
 CC receptors, T1R and their corresponding cDNA molecules. Taste receptors,
 CC T1R are useful for screening compounds which are used to activate or
 CC modulate chemosensory transduction, such as taste sensation. The
 CC identification and isolation of novel taste receptors and taste
 CC signalling molecules allow for new methods of chemical and genetic
 CC modulation of taste transduction pathways. The taste modulating compounds
 CC are useful in pharmaceuticals and food industries to improve the taste of
 CC a variety of consumer products, or to block undesirable tastes, e.g., in
 CC certain pharmaceuticals. T1R, s are also useful in biochemical assay for
 CC identifying tastant (T1R) ligands having binding specificity for T1R
 CC involved in taste signalling. The present sequence is human taste-cell-
 CC specific G protein-coupled receptor, hT1R3 full-length genomic DNA. Human
 CC T1R3 gene is localised on chromosome 1p36.2-1p36.33
 XX
 SQ Sequence 3563 BP; 545 A; 1214 C; 1166 G; 638 T; 0 U; 0 Other;
 Query Match 100.0%; Score 3563; DB 5; Length 3563;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 AGCCTGGCAGTGGCTCCTCAGGAGAGTCTGACCGGCACAACTTTAGGCCCGCAGGAGCGA 60
 1 AGCCTGGCAGTGGCTCCTCAGGAGAGTCTGACCGGCACAACTTTAGGCCCGCAGGAGCGA 60
 61 GGACACCACTGGGGCCCCAGGGTGTGGCAAGTGAGGTGGCAAGGGTTTGTCTAAACAAA 120
 61 GGACACCACTGGGGCCCCAGGGTGTGGCAAGTGAGGTGGCAAGGGTTTGTCTAAACAAA 120

QY 121 TCCTCTGCCGCTCCCGCGCCCGGGGTCACTCCATGTGAGGCCCGCCAGTCGGGGAGCCAC 180
 DB 121 TCCTCTGCCGCTCCCGCGCCCGGGGTCACTCCATGTGAGGCCCGCCAGTCGGGGAGCCAC 180
 QY 181 CTGCGGTGCGCTGTGGAAAGTTCCTCTGCGCATGCTGGGCCCTGCTGCTCTGGGCTCAGC 240
 DB 181 CTGCGGTGCGCTGTGGAAAGTTCCTCTGCGCATGCTGGGCCCTGCTGCTCTGGGCTCAGC 240
 QY 241 CTCTGGGCTCTCTCTGCACCCCTGGGAGCGGGGGCCCCCAATTGTGCTGTCAACAGCAACTTAGG 300
 DB 241 CTCTGGGCTCTCTCTGCACCCCTGGGAGCGGGGGCCCCCAATTGTGCTGTCAACAGCAACTTAGG 300
 QY 301 ATGAAGGGGACTACGTGCTGGGGGGGCTGTTCCTCCCTGGGCGAGGCGGAGGCTGSC 360
 DB 301 ATGAAGGGGACTACGTGCTGGGGGGGCTGTTCCTCCCTGGGCGAGGCGGAGGCTGSC 360
 QY 361 CTGCGAGCGGACACCGGCCACGAGCCCTGTGTGACACAGGTACAGAGTGGGACCGGCC 420
 DB 361 CTGCGAGCGGACACCGGCCACGAGCCCTGTGTGACACAGGTACAGAGTGGGACCGGCC 420
 QY 421 TGGGTCTGGGTTCAGGGTGACAGGTCTGGGGTGTCTCTGAGCTGGGGCCGAGGTGGCCAT 480
 DB 421 TGGGTCTGGGTTCAGGGTGACAGGTCTGGGGTGTCTCTGAGCTGGGGCCGAGGTGGCCAT 480
 QY 481 CTGCGGTCTGTGTGGGCCCGCAGGTCTCTCTCAACGCGCTGCTCTGGGCACTGGCCATGA 540
 DB 481 CTGCGGTCTGTGTGGGCCCGCAGGTCTCTCTCAACGCGCTGCTCTGGGCACTGGCCATGA 540
 QY 541 AATGGCCGTGGAGGAGATCAACAAAGTCGGATCTGTGCCCCGGGTGCGCCCTGGGCT 600
 DB 541 AATGGCCGTGGAGGAGATCAACAAAGTCGGATCTGTGCCCCGGGTGCGCCCTGGGCT 600
 QY 601 ACACCTCTTTGATACGTGCTCGGAGCTGTGGTGGCCATGAAGCCACGCTCATGTTC 660
 DB 601 ACACCTCTTTGATACGTGCTCGGAGCTGTGGTGGCCATGAAGCCACGCTCATGTTC 660
 QY 661 TGGCCAAAGGAGGAGCGGACATCGCGCTACTGCAACTACACGAGTACCGAGTACCAGCCC 720
 DB 661 TGGCCAAAGGAGGAGCGGACATCGCGCTACTGCAACTACACGAGTACCGAGTACCAGCCC 720
 QY 721 GTGTGCTGGCTGATCGGGCCCCACATCGTCAGAGCTCGCCATGCTGTCACCGGCAAGTTCT 780
 DB 721 GTGTGCTGGCTGATCGGGCCCCACATCGTCAGAGCTCGCCATGCTGTCACCGGCAAGTTCT 780
 QY 781 TCAGTCTTCTCTCATGCCAGTGGGGCGCCCCCACCACATCAACCCACCCCAACCAACC 840
 DB 781 TCAGTCTTCTCTCATGCCAGTGGGGCGCCCCCACCACATCAACCCACCCCAACCAACC 840
 QY 841 CCTGCCCGTGGAGGAGCCCTTGTGTGAGGAGAAATGCTACATGCAACCCACCCAGCCCTGC 900
 DB 841 CCTGCCCGTGGAGGAGCCCTTGTGTGAGGAGAAATGCTACATGCAACCCACCCAGCCCTGC 900
 QY 901 CCTGGAGCCCTGTGTGAGGAGTGTCTGTGGCTTGCAGGTGAGTACGCTGCTAGCAT 960
 DB 901 CCTGGAGCCCTGTGTGAGGAGTGTCTGTGGCTTGCAGGTGAGTACGCTGCTAGCAT 960
 QY 961 GGAGTCTGTGAGCGCCCGGAGACCTTCCCTCTCTTTCGCAACCGTCCCGAGGACCG 1020
 DB 961 GGAGTCTGTGAGCGCCCGGAGACCTTCCCTCTCTTTCGCAACCGTCCCGAGGACCG 1020
 QY 1021 TGTGAGTGTGAGCGCCCGGAGAGCTGTCAGAGAGTTCGGCTGGAATGGTGGTGGCCGC 1080
 DB 1021 TGTGAGTGTGAGCGCCCGGAGAGCTGTCAGAGAGTTCGGCTGGAATGGTGGTGGCCGC 1080
 QY 1081 CCTGGGAGCGACGACGAGTACGGCGCGGAGGCTGAGCATCTTCTCGGCTCTGGCCGC 1140
 DB 1081 CCTGGGAGCGACGACGAGTACGGCGCGGAGGCTGAGCATCTTCTCGGCTCTGGCCGC 1140
 QY 1141 GGCACGCGCATCTGATCGCGCACGAGGCGCTGCTGCGCTGCGCCCGTGGCGATGACTC 1200
 DB 1141 GGCACGCGCATCTGATCGCGCACGAGGCGCTGCTGCGCTGCGCCCGTGGCGATGACTC 1200
 QY 1201 GCGGCTGGGAGGAGTGGAGGAGCTCTCTGACAGGTGAACACGAGACGAGTGGAGTGT 1260

QY 3421 GCTGGGATCCCCCAGCCAGCAATGACCCGCTCTCTCGCTACAGAGACCTCCCGCTCT 3480
Db |||||
QY 3421 GCTGGGATCCCCCAGCCAGCAATGACCCGCTCTCTCGCTACAGAGACCTCCCGCTCT 3480
Db |||||
QY 3481 AGGTTCTGACCCAGCGTTGCTCTGACCTGACCCACAGTGAAGCCCTAGGCTGAGC 3540
Db |||||
QY 3481 AGGTTCTGACCCAGCGTTGCTCTGACCTGACCCACAGTGAAGCCCTAGGCTGAGC 3540
Db |||||
QY 3541 ACGTGGACACCCCTGTGACCATC 3563
Db |||||
QY 3541 ACGTGGACACCCCTGTGACCATC 3563
Db |||||
RESULT 2
ID ABN84919 standard; DNA; 3563 BP.
XX ABN84919;
AC ABN84919;
XX 25-NOV-2002 (first entry)
XX Human taste cell specific receptor hTIR3 genomic DNA.
XX hTIR3; TIR3; TIR; G-protein coupled receptor; receptor; human; taste;
KW sweet; gene; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
PH misc_feature 1..876
FT /tag= m
FT /note= "region specifically claimed in Claim 132"
FT CDS 211..3381
FT /tag= a
FT /product= "hTIR3"
FT exon 211..401
FT /tag= b
FT intron 402..502
FT /tag= c
FT exon 503..802
FT /tag= d
FT intron 803..939
FT /tag= e
FT misc_feature 877..3563
FT /tag= n
FT /note= "region specifically claimed in Claim 133"
FT exon 940..1723
FT /tag= f
FT intron 1724..1837
FT /tag= g
FT exon 1838..2041
FT /tag= h
FT intron 2042..2175
FT /tag= i
FT exon 2176..2296
FT /tag= j
FT intron 2297..2422
FT /tag= k
FT exon 2423..3381
FT /tag= l
XX WO200264631-A2.
XX 22-AUG-2002.
XX 03-JAN-2002; 2002WO-US000198.
XX 03-JAN-2001; 2001US-0259227P.
XX 19-APR-2001; 2001US-0284547P.
XX (SENO-) SENOMYX INC.
XX

PI Adler JE, Li X, Staszewski L, O'connell S, Zozulya S;
XX WPI; 2002-666991/71.
DR P-PSDB; ABB79827.
XX Novel mammalian taste-cell specific G protein-coupled receptors active in
PT taste signaling, useful for representing the perception of taste and for
PT predicting the perception of taste in a mammal.
XX Claim 1; Page 72-74; 132pp; English.
XX The present sequence is that of genomic DNA encoding a novel human G-
CC protein coupled receptor (GPCR), designated hTIR3, that is involved in
CC sweet taste transduction. The invention provides a new family of taste
CC cell-specific GPCRs, the TIRs, active in taste perception. Genomic DNAs
CC and cDNAs encoding the receptors are described, along with methods for
CC isolating TIR genes and for isolating and expressing TIR polypeptides.
CC Methods for representing taste perception of a particular taste stimulus
CC in a mammal, including a human, are also described, as are methods for
CC generating novel molecules or combinations of molecules that elicit a
CC predetermined taste perception in a mammal, and methods for stimulating
CC one or more tastes. Methods for stimulating or blocking taste perception
CC are also disclosed, as are methods of screening for modulators of these
CC novel taste cell-specific GPCRs. Such modulators are useful for
CC pharmacological, chemical and genetic modulation of taste signalling
CC pathways. They can be used in the food or pharmaceutical industries to
CC customize taste, e.g. to modulate the sweet tastes of foods or drugs. TIR
CC nucleic acids and the proteins they encode can be used as probes to
CC dissect taste-induced behaviours. Chromosome localisation of the genes
CC encoding human TIRs can be used to identify diseases, mutations, and
CC traits caused by and associated with TIR family members. TIR genes and
CC their homologues are useful tools for identifying chemosensory receptor
CC cells, for forensics and paternity determinations, and for examining
CC taste transduction
XX Sequence 3563 BP; 545 A; 1214 C; 1166 G; 638 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 3563; DB 6; Length 3563;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGGCAGTGGCTCAGGCAGAGTCTGACGCGCACAACTTTTCAGGCCAGGAGCGGA 60
Db |||||
QY 1 AGCTGGCAGTGGCTCAGGCAGAGTCTGACGCGCACAACTTTTCAGGCCAGGAGCGGA 60
Db |||||
QY 61 GGACACCACTGGGGCCCCCAGGGGTGTGGCAAGTGAAGATGGCAAGGTTTGTCTAAACAA 120
Db 61 GGACACCACTGGGGCCCCCAGGGGTGTGGCAAGTGAAGATGGCAAGGTTTGTCTAAACAA 120
QY 121 TCCTCTGCCGCTCCCCCGCCCGGGCTCACTTCATGTGAGGCCCCAGTCGGGGCAGCCAC 180
Db 121 TCCTCTGCCGCTCCCCCGCCCGGGCTCACTTCATGTGAGGCCCCAGTCGGGGCAGCCAC 180
QY 181 CTGCGGTGCTGTGGAAAGTTCCTCTGCCATGTCTGGGCCCTCTGTCTCTGGGCTCAGC 240
Db 181 CTGCGGTGCTGTGGAAAGTTCCTCTGCCATGTCTGGGCCCTCTGTCTCTGGGCTCAGC 240
QY 241 CTCTGGGCTCTCTCTGACCCCTGGGAGCGGGGCCCATTTGTGCTGTACAGCAACTTAGG 300
Db 241 CTCTGGGCTCTCTCTGACCCCTGGGAGCGGGGCCCATTTGTGCTGTACAGCAACTTAGG 300
QY 301 ATGAAGGGGGACTACGTCTGGGGGGGTGTTCCTCTGGGGAGCCCGAGGAGCTGGC 360
Db 301 ATGAAGGGGGACTACGTCTGGGGGGGTGTTCCTCTGGGGAGCCCGAGGAGCTGGC 360
QY 361 CTCGCCAGCCGACACAGGCCAGCCAGTGTGTGTGCACAGGTACAGAGTGGGAGCGCC 420
Db 361 CTCGCCAGCCGACACAGGCCAGCCAGTGTGTGTGCACAGGTACAGAGTGGGAGCGCC 420
QY 421 TGGGTGCGGGTTCAGGGTGACAGGTTCTGGGGTGTCTCTAGCTGGGGCCGAGGTGCCAT 480
Db 421 TGGGTGCGGGTTCAGGGTGACAGGTTCTGGGGTGTCTCTAGCTGGGGCCGAGGTGCCAT 480

QY 481 CTGGGTTCTGTGTGGCCCGCAGGTTCTCTAAACGGCCTGCTCTGGGCACTGGCCATGA 540
DB 481 CTGGGTTCTGTGTGGCCCGCAGGTTCTCTAAACGGCCTGCTCTGGGCACTGGCCATGA 540
QY 541 AAATGGCCGTGGAGGAGATCAACAACAAAGTCTGGATCTGTGCGCGGCTGGCTGGGCT 600
DB 541 AAATGGCCGTGGAGGAGATCAACAACAAAGTCTGGATCTGTGCGCGGCTGGCTGGGCT 600
QY 601 ACSACCTCTTTTGATACGTGTCTGGAGCCTGTGTGGCCATGAAGCCAGCCTCATGTTCC 660
DB 601 ACSACCTCTTTTGATACGTGTCTGGAGCCTGTGTGGCCATGAAGCCAGCCTCATGTTCC 660
QY 661 TGGCCAGGAGGAGGAGCCGCAATGCGCCGCTACTGCAACTACAGCAGTACAGAGCC 720
DB 661 TGGCCAGGAGGAGGAGCCGCAATGCGCCGCTACTGCAACTACAGCAGTACAGAGCC 720
QY 721 GTGTGCTGGTGTCTATCGGCGCCCACTCGTCAGAGCTCGCCATGTTCAACGGCAAGTTCT 780
DB 721 GTGTGCTGGTGTCTATCGGCGCCCACTCGTCAGAGCTCGCCATGTTCAACGGCAAGTTCT 780
QY 781 TCAGCTTCTTCTCATGCGCCCACTGGGCGCCCGCCCACTACACCCACCCCAACCAACC 840
DB 781 TCAGCTTCTTCTCATGCGCCCACTGGGCGCCCGCCCACTACACCCCAACCAACC 840
QY 841 CTTGCCCCGTGGAGGCCCCCTGTGTGTCAGAGAAATGTCTACATGCAACCCCAACCCCTGC 900
DB 841 CTTGCCCCGTGGAGGCCCCCTGTGTGTCAGAGAAATGTCTACATGCAACCCCAACCCCTGC 900
QY 901 CTTGGAGGCCCCCTGTGTGTCAGAGAAATGTCTTGGGCTTGGAGTCAAGTCTAGCAT 960
DB 901 CTTGGAGGCCCCCTGTGTGTCAGAGAAATGTCTTGGGCTTGGAGTCAAGTCTAGCAT 960
QY 961 GGAGCTGTGAGCGCCCGGAGACCTTCCCTCTTCTTCCGACCGTGCAGCGACCG 1020
DB 961 GGAGCTGTGAGCGCCCGGAGACCTTCCCTCTTCTTCCGACCGTGCAGCGACCG 1020
QY 1021 TGTGAGCTGACGGCCCGCGGAGCTGTGTGTCAGAGAAATGTGTGGTGGCCGC 1080
DB 1021 TGTGAGCTGACGGCCCGCGGAGCTGTGTGTCAGAGAAATGTGTGGTGGCCGC 1080
QY 1081 CTTGGGACGACGACGAGTACGGCGGCGAGGCTGTGTCAGAGAAATGTGTGGTGGCCGC 1140
DB 1081 CTTGGGACGACGACGAGTACGGCGGCGAGGCTGTGTCAGAGAAATGTGTGGTGGCCGC 1140
QY 1141 GGCACGGGCACTGTGATCGGCAACGAGGCTGTGTGTCAGAGAAATGTGTGGTGGCCGC 1200
DB 1141 GGCACGGGCACTGTGATCGGCAACGAGGCTGTGTGTCAGAGAAATGTGTGGTGGCCGC 1200
QY 1201 GGGGCTGGGAGGTCAGGAGCTGTGTCAGAGAAATGTGTGGTGGCCGC 1260
DB 1201 GGGGCTGGGAGGTCAGGAGCTGTGTCAGAGAAATGTGTGGTGGCCGC 1260
QY 1261 GGTGCTGTGCGCTCCGTGTCAGCGCCGCGAGGCTGTGTGTCAGAGAAATGTGTGGTGGCCGC 1320
DB 1261 GGTGCTGTGCGCTCCGTGTCAGCGCCGCGAGGCTGTGTGTCAGAGAAATGTGTGGTGGCCGC 1320
QY 1321 GCTCTGCGCCAAAGTGTGGTGGCCGAGGCTGTGTGTCAGAGAAATGTGTGGTGGCCGC 1380
DB 1321 GCTCTGCGCCAAAGTGTGGTGGCCGAGGCTGTGTGTCAGAGAAATGTGTGGTGGCCGC 1380
QY 1381 GCTGCGCGGCAATGGCCAGATGGGACGCTGTGTGTCAGAGAAATGTGTGGTGGCCGC 1440
DB 1381 GCTGCGCGGCAATGGCCAGATGGGACGCTGTGTGTCAGAGAAATGTGTGGTGGCCGC 1440
QY 1441 GCACGAGTTCCTCCAGTACGTGAGAGCAGCTGTGTCAGAGAAATGTGTGGTGGCCGC 1500
DB 1441 GCACGAGTTCCTCCAGTACGTGAGAGCAGCTGTGTCAGAGAAATGTGTGGTGGCCGC 1500
QY 1501 CTTGCCCCGTGGAGGAGGAGGCTGTGTCAGAGAAATGTGTGGTGGCCGC 1560
DB 1501 CTTGCCCCGTGGAGGAGGAGGCTGTGTCAGAGAAATGTGTGGTGGCCGC 1560
QY 1561 GCAGTGTGCTGATCATCGCTGTCAGAACTGTGAGCGGCTAAATCATCAACCAAGCCTT 1620

DB 1561 GCAGTGTGCTGATCATCGCTGTCAGAACTGTGAGCGGCTAAATCATCAACCAAGCCTT 1620
QY 1621 CTTGCTCTACGAGCTGTGTATAGCTGGCCCGGCTGTGCAACAACTCTTCACTGCAAA 1680
DB 1621 CTTGCTCTACGAGCTGTGTATAGCTGGCCCGGCTGTGCAACAACTCTTCACTGCAAA 1680
QY 1681 CGGCTCAGGCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1740
DB 1681 CGGCTCAGGCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1740
QY 1741 GGGTGTGTGTCTCTGCTGATGTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1800
DB 1741 GGGTGTGTGTCTCTGCTGATGTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1800
QY 1801 AGGTGCTGGGCTCAGGCTGCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1860
DB 1801 AGGTGCTGGGCTCAGGCTGCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1860
QY 1861 GACCTTCCAGCTGGGCGGCTGCGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920
DB 1861 GACCTTCCAGCTGGGCGGCTGCGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920
QY 1921 GTACGACCTCAAGCTGTGGTGTGGCAGGCTCAGTGGCCGAGGCTCCAGGAGCTGGGAG 1980
DB 1921 GTACGACCTCAAGCTGTGGTGTGGCAGGCTCAGTGGCCGAGGCTCCAGGAGCTGGGAG 1980
QY 1981 GTTCAACGGGAGCTCAGGAGAGGCTGCTGAGAGTCCGCTGSCACACCTGTGCAACCA 2040
DB 1981 GTTCAACGGGAGCTCAGGAGAGGCTGCTGAGAGTCCGCTGSCACACCTGTGCAACCA 2040
QY 2041 GGTGAGGTCAGGCTGGTGTGCGGAGGCTGCGGCTGCGGAGGCTGCGGAGGCTGCGGAGG 2100
DB 2041 GGTGAGGTCAGGCTGGTGTGCGGAGGCTGCGGCTGCGGAGGCTGCGGAGGCTGCGGAGG 2100
QY 2101 CTGGGCTGGGCGGCTTCCAGTCTCCGCTGGGAGTCCGAGCCGAGGAGGAGGAGGAGGAGG 2160
DB 2101 CTGGGCTGGGCGGCTTCCAGTCTCCGCTGGGAGTCCGAGCCGAGGAGGAGGAGGAGGAGG 2160
QY 2161 CAGGCTGTGCGCAAGGCTGCTGCGGAGGCTGCGGAGGCTGCGGAGGCTGCGGAGGCTGCGGAGG 2220
DB 2161 CAGGCTGTGCGCAAGGCTGCTGCGGAGGCTGCGGAGGCTGCGGAGGCTGCGGAGGCTGCGGAGG 2220
QY 2221 GCGCGGCTCAAGGCTTCCAGTCTCCGCTGGGAGTCCGAGCCGAGGAGGAGGAGGAGGAGG 2280
DB 2221 GCGCGGCTCAAGGCTTCCAGTCTCCGCTGGGAGTCCGAGCCGAGGAGGAGGAGGAGGAGG 2280
QY 2281 TACCGGCAAAACCCAGGTCAGGCTGCTCCGCGGAGGCGGCGGCTGGGAGGAGGAGGAGGAGG 2340
DB 2281 TACCGGCAAAACCCAGGTCAGGCTGCTCCGCGGAGGCGGCGGCTGGGAGGAGGAGGAGGAGG 2340
QY 2341 AGGCTCTGCGCAAGTCTGATCTGTGAGACAGAGCCCAAGGCTACAGAGGAGGAGGAGGAGGAGG 2400
DB 2341 AGGCTCTGCGCAAGTCTGATCTGTGAGACAGAGCCCAAGGCTACAGAGGAGGAGGAGGAGGAGG 2400
QY 2401 GCGGCTCTCTCTCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2460
DB 2401 GCGGCTCTCTCTCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2460
QY 2461 TCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2520
DB 2461 TCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2520
QY 2521 CCGGCTGTGCTGTGCTCTCTCTGCTGAGGCTGCGGCTGGGCTGTGCTGTGCTGTGCTGTGCTGTGCT 2580
DB 2521 CCGGCTGTGCTGTGCTCTCTCTGCTGAGGCTGGGCTGGGCTGTGCTGTGCTGTGCTGTGCTGTGCT 2580
QY 2581 TTGGGCTGTGCTGTGCTCTCTCTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2640
DB 2581 TTGGGCTGTGCTGTGCTCTCTCTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2640
QY 2641 GCCTGCTTTGGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 2700

Db	2641	GCCTGCTTTGGCCTCGTGTGCTGGCTGGGCTGTGCTCTCAGCGTCTCTCTGTTCCTCTGGC	2700
Qy	2701	CAGCCAGCCCTGCCGATGCTGCTGGCCAGACAGCCCTTGTCCACTCTCCGCTCACGGGC	2760
Db	2701		
Db	2701	CAGCCAGCCCTGCCGATGCTTGGCCAGACAGCCCTTGTCCACTCTCCGCTCACGGGC	2760
Qy	2761	TGCCTGAGCACACTCTTCTCTGAGGCGGCCGAGATCTTGTGGAGTCAGAACTGCCTCTG	2820
Db	2761		
Db	2761	TGCCTGAGCACACTCTTCTCTGAGGCGGCCGAGATCTTGTGGAGTCAGAACTGCCTCTG	2820
Qy	2821	AGTGGGCAGACCGGTGAGTGGCTGTGCTGGGGGGCCCTGGGCTGGTGGTGTGCTG	2880
Db	2821		
Db	2821	AGTGGGCAGACCGGTGAGTGGCTGTGCTGGGGGGCCCTGGGCTGGTGGTGTGCTG	2880
Qy	2881	CTGGCCATGCTGTTGAGGTGCACACTGTACTCTGTGGCCTTCCCGCCGGAG	2940
Db	2881		
Db	2881	CTGGCCATGCTGTTGAGGTGCACACTGTACTCTGTGGCCTTCCCGCCGGAG	2940
Qy	2941	GTGCTGACGACTTGGCACATGCTTGGCCACGAGAGCGCTGTGCACCTGCCGACACGCTCC	3000
Db	2941		
Db	2941	GTGCTGACGACTTGGCACATGCTTGGCCACGAGAGCGCTGTGCACCTGCCGACACGCTCC	3000
Qy	3001	TGGGTGAGCTTGGCCTTAGGCAAGCCACCAATGCCACGCTGGCCTTCTCTGCTTCCCTG	3060
Db	3001		
Db	3001	TGGGTGAGCTTGGCCTTAGGCAAGCCACCAATGCCACGCTGGCCTTCTCTGCTTCCCTG	3060
Qy	3061	GGCACTTTCCTGTGGAGCCAGCCAGCGGGCTGTCAACCGTGGCGCTTCTGCTTCCCTTT	3120
Db	3061		
Db	3061	GGCACTTTCCTGTGGAGCCAGCCAGCGGGCTGTCAACCGTGGCGCTTCTGCTTCCCTTT	3120
Qy	3121	GCCATGCTGCCTTACTTTCATCAGCTGGGTCTCTCTTTGTGCCCTCTCTGCCAATGTGCAG	3180
Db	3121		
Db	3121	GCCATGCTGCCTTACTTTCATCAGCTGGGTCTCTCTTTGTGCCCTCTCTGCCAATGTGCAG	3180
Qy	3181	GTGCTCTCAGGCCCGCGTGCAGATGGGGCCCTCTGTGCTGTGTCTCTGGGCATCTCTG	3240
Db	3181		
Db	3181	GTGCTCTCAGGCCCGCGTGCAGATGGGGCCCTCTGTGCTGTGTCTCTGGGCATCTCTG	3240
Qy	3241	GCTGCTTCCACCTGCCAGGTGTACTGCTCATGCGGAGCAGGGCTCAACACCCCC	3300
Db	3241		
Db	3241	GCTGCTTCCACCTGCCAGGTGTACTGCTCATGCGGAGCAGGGCTCAACACCCCC	3300
Qy	3301	GAGTTCTCTGGAGGGGGCCCTGGGGATGCCCCAAGGCCAGATGACGGGAACACAGGA	3360
Db	3301		
Db	3301	GAGTTCTCTGGAGGGGGCCCTGGGGATGCCCCAAGGCCAGATGACGGGAACACAGGA	3360
Qy	3361	AATCAGGGGAAACATGAGTGACCCAAACCTCTGTGATCTCAGCCCGGGTGAAACCCAGCTTA	3420
Db	3361		
Db	3361	AATCAGGGGAAACATGAGTGACCCAAACCTCTGTGATCTCAGCCCGGGTGAAACCCAGCTTA	3420
Qy	3421	GCTGCGATCCCCCAGACGCAAGTAACCCGTGTCTCGTGTACAGAGACCTCTCCCGCTCT	3480
Db	3421		
Db	3421	GCTGCGATCCCCCAGACGCAAGTAACCCGTGTCTCGTGTACAGAGACCTCTCCCGCTCT	3480
Qy	3481	AGGTTCTGACCCCGAGTTGTCTCTGACCTTGACCCCAAGTAGTGAGCCCTTAGGCTGGAGC	3540
Db	3481		
Db	3481	AGGTTCTGACCCCGAGTTGTCTCTGACCTTGACCCCAAGTAGTGAGCCCTTAGGCTGGAGC	3540
Qy	3541	ACGTGGACACCCCTGTGACCAATC	3563
Db	3541		
Db	3541	ACGTGGACACCCCTGTGACCAATC	3563

RESULT 3	
AAL38463	
ID AAL38463 standard; DNA; 8001 BP.	
XX AC	(PEKE) PE CORP NY.
XX AC	Wei M, Zhong W, Ketchum KA, DiFrancesco V, Beasley EM;
XX AC	WPI; 2002-444173/47.
DT 15-AUG-2002 (first entry)	P-PADB; AAC21501.
XX	Novel G protein coupled receptor, useful for raising antibodies, to
DE Genomic DNA encoding a human G-protein coupled receptor (GPCR).	elicite immune response, and as a reagent in assays designed to
XX	

quantitatively determine levels of protein in biological samples.

Disclosure; Fig 3; 82pp; English.

The invention relates to an isolated G-protein coupled receptor (GPCR) polypeptide, comprising an 852 residue amino acid sequence, given in the specification, an allelic variant or ortholog of the protein, or a fragment comprising at least 10 contiguous amino acids of the protein. GPCR is useful for identifying a modulator of GPCR and an agent that binds to GPCR. GPCR and a gene chip comprising GPCR are useful as models for the development of human therapeutic agents. GPCR is useful for raising antibodies, to elicit immune response, as a reagent in assays designed to quantitatively determine levels of protein in biological samples, and as markers for tissues in which the corresponding protein is preferentially expressed. A gene chip containing GPCR is also useful as a probe for determining the chromosomal positions of nucleic acid molecules by means of in situ hybridisation, in making vectors containing the gene regulatory regions of a gene chip containing GPCR, for designing ribozymes, in making vectors that express GPCR, and for constructing host cells and transgenic animals expressing nucleic acid molecules and peptides. A host cell containing GPCR is useful for conducting cell-based assays involving GPCR protein or its fragments, and for identifying protein mutants in which these function is affected. For identifying encoding GPCR can be used to treat disorders by gene therapy. The polynucleotide sequence represents the genomic DNA encoding the human G-protein coupled receptor of the invention

Sequence 8001 BP; 1291 A; 2630 C; 2623 G; 1457 T; 0 U; 0 Other;

ry Match 95.5%; Score 3403.8; DB 6; Length 8001;

Local Similarity 97.9%; Pred. No. 0;
ches 3489; Conservative 0; Mismatches 22; Indels 52.

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RESULT 4
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 ID ACA62667 standard; cDNA; 8001 BP.
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 XX 19-AUG-2003 (first entry)
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 XX DNA encoding human calcium sensing G-protein coupled receptor.
 DE Human; ds; gene; GPCR; G-protein coupled receptor; gene therapy;
 XX Parkinson's disease; Huntington's disease; Tourette's syndrome; SNP;
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XX WPI; 2003-492117/46.
XX P-PSDB; AB062106.
XX
XX New isolated human G-protein coupled receptor proteins, useful for
XX treating e.g. Parkinson's disease, Huntington's disease or Tourette's
XX syndrome, or for developing human therapeutics and diagnostic

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PT      compositions.
XX      Claim 4; Fig 3A-3C; 46pp; English.
XX
CC      The invention relates to an isolated human G-protein coupled receptor
CC      (GPCR) peptide. The human GPCR peptides and nucleic acid molecules are
CC      useful in the development of human therapeutics and diagnostic
CC      compositions. The peptides are useful for treating disorders (e.g.
CC      Parkinson's disease, Huntington's disease or Tourette's syndrome)
CC      characterised by an absence of, inappropriate, or unwanted expression of
CC      the GPCR protein, or disorders mediated by proteases. These molecules are
CC      particularly useful as models for developing human therapeutic targets,
CC      identifying therapeutic proteins, or serving as targets for the
CC      development of human therapeutic agents that modulate GPCR activity in
CC      cells and tissues that express the GPCR. The peptides are also useful for
CC      raising antibodies or eliciting an immune response, as a reagent
CC      (including the labelled reagent) in assays designed to quantitatively
CC      determine levels of the protein (or its binding partner or ligand) in
CC      biological fluids, or as markers for tissues in which the corresponding
CC      protein is preferentially expressed. The agents identified are useful for
CC      treating a subject with a disorder mediated by human proteases. The
CC      present sequence represents DNA encoding human calcium sensing G-protein
CC      coupled receptor
XX
XX      Sequence 8001 BP; 1291 A; 2632 C; 2623 G; 1455 T; 0 U; 0 Other;
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 QY 2377 CACAGGGTACAAGACGAAACACCCAGCGCCCTTCTCTCTCTCAACAGACGATCGCCTGC 2436
 Db 1501 CACAGGGTACAAGACGAAACACCCAGCGCCCTTCTCTCTCTCAACAGACGATCGCCTGC 1560
 QY 2437 ACCTTTTGTGGCAGAGATGAGTGTCCCGAGGAGGACACACGCTGCTCCCGCGCAGG 2496
 Db 1561 ACCTTTTGTGGCAGAGATGAGTGTCCCGAGGAGGACACACGCTGCTCCCGCGCAGG 1620
 QY 2497 TCTCGGTTCCTGGCATGGGCGAGCGCTGTGCTGTGCTGTCTCTCTCTCTCTGAGCCTG 2556
 Db 1621 TCTCGGTTCCTGGCATGGGCGAGCGCTGTGCTGTGCTGTCTCTCTCTCTCTGAGCCTG 1680
 QY 2557 GCGCTGCGCCTTGTGCTGTGCTTTTGGGGGTGTTCGTTTCAACATCGGAGACGCGCCTG 2616
 Db 1681 GCGCTGCGCCTTGTGCTGTGCTTTTGGGGGTGTTCGTTTCAACATCGGAGCAGCGCCTG 1740
 QY 2617 GTTCAGGCTTCGGGGGCGCCCTGCGCTGCTTTTGGCGTGTGCTGCTGCGGCTGTCTGTC 2676
 Db 1741 GTTCAGGCTTCGGGGGCGCCCTGCGCTGCTTTTGGCGTGTGCTGCTGCGGCTGTCTGTC 1800
 QY 2677 CTCAGGCTTCCTGCTTCCCTGGCCAGCCAGCGCCCTGCCGATGCTGGCCAGCAGCGCC 2736
 Db 1801 CTCAGGCTTCCTGCTTCCCTGGCCAGCCAGCGCCCTGCCGATGCTGGCCAGCAGCGCC 1860
 QY 2737 TTGTCCCACTCCCGCTCAGCGGCTGCTGAGCACTTCTTCTGCGAGCGCGCGAGATC 2796
 Db 1861 TTGTCCCACTCCCGCTCAGCGGCTGCTGAGCACTTCTTCTGCGAGCGCGCGAGATC 1920
 QY 2797 TTCGTGAGTCAAGAACTGCTCTCAGCTGGCGAGACCGGCTGAGTGGCTGCTGCGGGG 2856
 Db 1921 TTCGTGAGTCAAGAACTGCTCTCAGCTGGCGAGACCGGCTGAGTGGCTGCTGCGGGG 1980
 QY 2857 CCCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2916
 Db 1981 CCCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
 QY 2917 TACCTGTGGCTTCTCCCGCGAGGTGTGCGGATGCTGCGCACTGCTGCGCAGGAGCG 2976
 Db 2041 TACCTGTGGCTTCTCCCGCGAGGTGTGCGGATGCTGCGCACTGCTGCGCAGGAGCG 2100
 QY 2977 CTGCTGCTGCGCAGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3036
 Db 2101 CTGCTGCTGCGCAGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
 QY 3037 AGCTGGGCTTCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3096
 Db 2161 AGCTGGGCTTCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
 QY 3097 AACCTGCGCGGCTCTCACTTTGCGCATGCTGGGCTTCTTCTGCTGCTGCTGCTGCTGCT 3156
 Db 2221 AACCTGCGCGGCTCTCACTTTGCGCATGCTGGGCTTCTTCTGCTGCTGCTGCTGCTGCT 2280
 QY 3157 GTGCCCCCTCTGCGCAATGCTGAGGTGCTCTCAGGCGCGGCTGCTGAGATGGGCGCGCTC 3216

Db 2281 GTGCCCCCTCTGSCCAATGTCAGGTGGTCTCAGGCCCGCCGTCAGATGGGCGCCCTC 2340
 QY 3217 CTGCTCTGTCTCTGGGCATCTTGGCTGCTTCCACCTGCCAGGTGTACCTGCTCATG 3276
 Db 2341 CTGCTCTGTCTCTGGGCATCTTGGCTGCTTCCACCTGCCAGGTGTACCTGCTCATG 2400
 QY 3277 CGCAGCAGGGCTCAACACCCCGAGTTCCTTCTGGGAGGGGGCCCTGGGGATGCCCAA 3336
 Db 2401 CGCAGCAGGGCTCAACACCCCGAGTTCCTTCTGGGAGGGGGCCCTGGGGATGCCCAA 2460
 QY 3337 GGCAGATACAGGGACACAGAGAAATCAGGGAACATGAGTGACCCCAACCTGTGATC 3396
 Db 2461 GGCAGATACAGGGAAACACAGAGAAATCAGGGAACATGAGTGACCCCAACCTGTGATC 2520
 QY 3397 TCAGCCCCGGTGAACCCAGACTTAGCTGCGATCCCGCCCAAGCCAGCAATGACCCGTGTC 3456
 Db 2521 TCAGCCCCGGTGAACCCAGACTTAGCTGCGATCCCGCCCAAGCCAGCAATGACCCGTGTC 2580
 QY 3457 TGCTACAGAGACCCCTCCGCTTAGGTTCTGACCCCGAGTTCCTCTGACCCGTGACCC 3516
 Db 2581 TGCTACAGAGACCCCTCCGCTTAGGTTCTGACCCCGAGTTCCTCTGACCCGTGACCC 2640
 QY 3517 CACAGTGACCCCTAGCCTGGACACGTCGACACCCCTGTGACCATC 3563
 Db 2641 CACAGTGACCCCTAGCCTGGACACGTCGACACCCCTGTGACCATC 2687

RESULT 9

AD140945
 ID AD140945 standard; cDNA; 2685 BP.
 XX AD140945;
 AC AD140945;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human G protein-coupled receptor HGPRMWY30_3 cDNA.

XX Human; ss; gene; GPCR; G protein-coupled receptor; reproductive disorder;
 KW testicular disorder; vas deferens disorder; spermatogenesis; infertility;
 KW XX male; epididymitis; cryptorchidism; sperm transport disorder;
 KW testicular cancer; testicular germ cell tumour; male hormone disorder;
 KW premature puberty; Kallman syndrome; Cushing's syndrome; immune disorder;
 KW leukaemia; arthritis; asthma; AIDS; rheumatoid arthritis;
 KW inflammatory bowel disease; sepsis; T-cell mediated cytotoxicity;
 KW graft-versus-host disease; autoimmunity disorder;
 KW systemic lupus erythematosus; drug induced haemolytic anaemia;
 KW Sjogren's disease; T-cell maturation disorder;
 KW B-cell maturation disorder; vascular disorder; stroke; ischaemia;
 KW myocardial infarction; atherosclerosis; gastrointestinal disorder; ulcer;
 KW pulmonary disorder; brain disorder; endocrine disorder; cancer;
 KW gene therapy.

XX Homo sapiens.

OS
 XX US2004018976-A1.

PN
 XX 29-JAN-2004.

PD
 XX 13-MAY-2003; 2003US-00436715.

PF
 XX 14-MAY-2002; 2002US-0380336P.

PR
 XX (FEDE/) FEDER J N.
 PA (MINT/) MINTIER G.
 PA (RAMA/) RAMANATHAN C S.

PI Feder JN, Mintier G, Ramanathan CS;

XX WPI; 2004-122081/12.
 DR P-PSDB; AD140946.

XX New human G-protein coupled receptor polypeptide and polynucleotide,
 PT

useful for diagnosing, preventing, treating or ameliorating a medical condition, e.g. reproductive disorder, immunodeficiency disease or testicular cancer.

Claim 1; SEQ ID NO 5; 290pp; English.

The invention relates to an isolated human G protein-coupled receptor polypeptide and its encoding polynucleotide, including the full length proteins minus the start methionine (and the region of the polynucleotide encoding this protein region). The proteins are designated HGPRMWY30-1, HGPRMWY30-2, HGPRMWY30-3, HGPRMWY41-1, HGPRMWY41-2, HGPRMWY41-3, HGPRMWY42, HGPRMWY42-1, HGPRMWY43 and HGPRMWY44. Also included are expression vectors, host cells, antibodies, preventing (treating or ameliorating) a medical condition comprising administering to a mammalian subject the polypeptide or its modulator and diagnosing a pathological condition or a susceptibility to a pathological condition in a subject (comprising determining the presence or absence of a mutation in the polynucleotide, or the presence or amount of expression of the polypeptide in a biological sample and diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of the mutation, or the presence or amount of expression of the polypeptide). The human G-protein coupled receptor polypeptide or polynucleotide can be used for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, and for preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant G-protein coupled receptor activity, a disorder related to aberrant signal transduction, a reproductive disorder; a male reproductive disorder, a testicular disorder, a vas deferens disorder, spermatogenesis, infertility, Klinefelter's syndrome, XX male, epididymitis, genital warts, germinal cell aplasia, cryptorchidism, varicocele, immotile cilia syndrome, viral orchitis, sperm transport disorders, testicular cancer, choriocarcinoma, non-seminoma, seminoma, testicular germ cell tumours, male hormone disorders, premature puberty, incomplete puberty, Kallman syndrome, Cushing's syndrome, an immune disorder, a proliferative immune disorder, leukaemia, arthritis, asthma, immunodeficiency diseases such as AIDS, rheumatoid arthritis, granulomatous disease, inflammatory bowel disease, sepsis, acne, neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell mediated cytotoxicity, immune reactions to transplanted organs and tissues, such as host-versus-graft and graft-versus-host diseases, or autoimmunity disorders, such as autoimmune infertility, demyelination, systemic lupus erythematosus, drug induced haemolytic anaemia, Sjogren's disease, scleroderma, T-cell maturation disorders, B-cell maturation disorders, vascular disorders, stroke, ischaemia, myocardial infarction, atherosclerosis, embolisms, thrombosis, gastrointestinal disorders, irritable bowel syndrome, ulcers, pulmonary disorders, brain disorders, endocrine disorders, or ovarian, stomach, colon or kidney cancer or its related proliferative condition (many other diseases and disorders are listed in the specification). The antibodies may be used to purify, detect and target the G-protein coupled receptor polypeptides. The polynucleotides are also useful in gene therapy. The present sequence encodes a novel GPCR of the invention.

Sequence 2685 BP; 404 A; 906 C; 882 G; 493 T; 0 U; 0 Other;

Query Match 60.6%; Score 2157.4; DB 12; Length 2685;
 Best Local Similarity 84.6%; Fred. No. 0;
 Matches 2684; Conservative 0; Mismatches 1; Indels 486; Gaps 4;

QY 211 ATGCTGGGCCCTGTGCTCTGGGCTCAGCCTCTGGGCTCTCTGACCCCTGGGAGGGG 270
 Db 1 ATGCTGGGCCCTGTGCTCTGGGCTCAGCCTCTGGGCTCTCTGACCCCTGGGAGGGG 60
 QY 271 GCCCATTTGTCCTGTCTACACAACTTAGTAGTAAGGGGGACTACGTCTGGGGGGCTG 330
 Db 61 GCCCATTTGTCCTGTCTACACAACTTAGTAGTAAGGGGGACTACGTCTGGGGGGCTG 120
 QY 331 TTCCCCCTGGGCGAGGCGAGGAGGCTGGCCCTCCGACCGCGGACACGGCCCGAGGCCCT 390
 Db 121 TTCCCCCTGGGCGAGGCGAGGAGGCTGGCCCTCCGACCGCGGACACGGCCCGAGGCCCT 180
 QY 391 GTGTGCACACAGGTACAGAGGTGGGACGCGCTGGGTTCGGGGTTCAGGGTGACCAAGTCTGGG 450
 XX |||||

QY	2611	CCACTGGTTACAGGCTTCGGGGGGCCCTGGGCTTGTCTTTGGCTGTGTGTGCTTGGGCTGTG	2670
Db	1915	CCACTGGTTACAGGCTTCGGGGGGCCCTGGGCTTGTCTTTGGCTGTGTGTGCTTGGGCTGTG	1974
QY	2671	GTCTGGCTCAGCGTCTCTCTGTTCCTTGGCCAGGCCAGCCCTGCCCGAGTGCCTGGCCAG	2730
Db	1975	GTCTGGCTCAGCGTCTCTCTGTTCCTTGGCCAGGCCAGCCCTGCCCGAGTGCCTGGCCAG	2034
QY	2731	CAGCCCTTGTGCCACCTCCCGCTCACGGGCTGCCTGAGCACACATCTCTTCGACGGCGGCC	2790
Db	2035	CAGCCCTTGTGCCACCTCCCGCTCACGGGCTGCCTGAGCACACATCTCTTCGACGGCGGCC	2094
QY	2791	GAGATCTTCGTGGAGTACAGAACTGCCTCTGAGCTGGGAGACCCGGCTGAGTGGCTGCCTG	2850
Db	2095	GAGATCTTCGTGGAGTACAGAACTGCCTCTGAGCTGGGAGACCCGGCTGAGTGGCTGCCTG	2154
QY	2851	CGGGGGCCCTGGGCTGTGCTGTGTCTGTGCGCATGCTGTGTGTGTGTGTGTGTGTGTGTGT	2910
Db	2155	CGGGGGCCCTGGGCTGTGCTGT	2214
QY	2911	ACCTGGTACCTGTGTGGCTTCCCGCCGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2970
Db	2215	ACCTGGTACCTGTGTGGCTTCCCGCCGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2274
QY	2971	GAGGCGCTGTGTGCATGCTGCCGACACGCTCTCTGGGTGAGCTTCGGGCTAGCGGACGCCACC	3030
Db	2275	GAGGCGCTGTGTGCATGCTGCCGACACGCTCTCTGGGTGAGCTTCGGGCTAGCGGACGCCACC	2334
QY	3031	AATGCCAGCTGGCTTCTCTGTCTTCTGTGGGCACTTTTCTGTGTGTGTGTGTGTGTGTGTGT	3090
Db	2335	AATGCCAGCTGGCTTCTCTGTCTTCTGTGGGCACTTTTCTGTGTGTGTGTGTGTGTGTGTGT	2394
QY	3091	TGCTACAACTGCGCGTGGGCTCACCTTTGGCATGCTGGGCTGAGCTTCGGGCTAGCGGACGCCACC	3150
Db	2395	CGCTACAACTGCGCGTGGGCTCACCTTTGGCATGCTGGGCTGAGCTTCGGGCTAGCGGACGCCACC	2454
QY	3151	TCCTTTGTGCCCTCTCTGGGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	3210
Db	2455	TCCTTTGTGCCCTCTCTGGGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2514
QY	3211	GCCCTCTGTCTGTGTCTGTGGGATCCTGGCTGCCTTCCACTGCCAGAGTGTACCTGTG	3270
Db	2515	GCCCTCTGTCTGTGTCTGTGGGATCCTGGCTGCCTTCCACTGCCAGAGTGTACCTGTG	2574
QY	3271	CTCATGGGAGCCAGGAGCTCAACACCCCGAGTCTTCTCTGGAGGGGCGCTTGGGGAT	3330
Db	2575	CTCATGGGAGCCAGGAGCTCAACACCCCGAGTCTTCTCTGGAGGGGCGCTTGGGGAT	2634
QY	3331	GCCCAAGGCCAGATGACGGGAAACACAGGAAATCAGGGGAAACATGAGTGA	3381
Db	2635	GCCCAAGGCCAGATGACGGGAAACACAGGAAATCAGGGGAAACATGAGTGA	2685
RESULT 10			
AAS14574			
ID	AAS14574 standard; cDNA; 3489 BP.		
XX	AAS14574;		
AC			
XX			
DT	18-DEC-2001 (first entry)		
XX	Human cDNA encoding G protein-coupled receptor, GPCR, 50289.		
DE			
XX			
KW	Human; ss; GPCR; G protein-coupled receptor; 50289; cardiant;		
KW	antiatherosclerotic; analgesic; cytosolic; antianginal;		
KW	cardiovascular disorder; angiogenesis-related disorder; neural disorder;		
KW	pain response disorder; inflammatory disorder; atherosclerosis;		
KW	angina pectoris; myocardial infarction; ischaemic heart disease;		
KW	sudden cardiac death; obesity; hypertensive heart disease; diabetes;		
KW	prostate cancer-related pain.		
OS	Homo sapiens.		
XX			

Db 270 ACTGGCCATGAARATGSCCGTGGAGGAGATCAACAAACAGTCGGATCTGCTGCCCGGCT 329
 Qy 590 GCGCTGGGTACAGACCTCTTTGATAGTGTGGAGCCTGTGTGGCCATGAAGCCAG 649
 Db 330 GCGCTGGGTACAGACCTCTTTGATAGTGTGGAGCCTGTGTGGCCATGAAGCCAG 389
 Qy 650 CCTCATGTTCTTGGCCAAAGCAGCAGCGGACATCGCGCTTACTGCAACTACAGCA 709
 Db 390 CCTCATGTTCTTGGCCAAAGCAGCAGCGGACATCGCGCTTACTGCAACTACAGCA 449
 Qy 710 GTACACGCCCGTGTGTGGTGTGTCATCGGCCCCACTCGTCAGAGCTGCGCATGCTAC 769
 Db 450 GTACACGCCCGTGTGTGGTGTGTCATCGGCCCCACTCGTCAGAGCTGCGCATGCTAC 509
 Qy 770 CGGCAAGTCTTACAGTCTTCTCTCATGCCCCAGTGGGGCCCCCACCACCATCACCCACC 829
 Db 510 CGGCAAGTCTTACAGTCTTCTCTCATGCCCCAGTGGGGCCCCCACCACCATCACCCACC 540
 Qy 830 CCCAACCAACCCCTGCCCGTGGGAGCCCTTGTGTGTCAGGAGATGCTTACATGCACCCCA 889
 Db 541 ----- 540
 Qy 890 CCCAGCCCTGCTGGAGCCCTGTGTGTCAGGAGATGCTTGGGCTTGCAGGTACAGTAC 949
 Db 541 ----- CAGGTACAGTAC 552
 Qy 950 GGTGTAGCATGGAGCTGCTGAGCGCCCGGAGACCTTCCCTCTTCCGACACCGTG 1009
 Db 553 GGTGTAGCATGGAGCTGCTGAGCGCCCGGAGACCTTCCCTCTTCCGACACCGTG 612
 Qy 1010 CCCAGCACCTGTGTGACCTGACGCGCCCGGAGCTGCTGCGAGAGTTCGGTGGAAAC 1069
 Db 613 CCCAGCACCTGTGTGACCTGACGCGCCCGGAGCTGCTGCGAGAGTTCGGTGGAAAC 672
 Qy 1070 TGGGTGGCGGCTTGGGAGCGACGACGAGTACGCGCGGAGGCTGAGCATCTTCTCG 1129
 Db 673 TGGGTGGCGGCTTGGGAGCGACGACGAGTACGCGCGGAGGCTGAGCATCTTCTCG 732
 Qy 1130 GCGCTGGCGGAGCGGACCTGTCATCGCGACGAGGCTGCTGGCGGCTGCCCGT 1189
 Db 733 GCGCTGGCGGAGCGGACCTGTCATCGCGACGAGGCTGCTGGCGGCTGCCCGT 792
 Qy 1190 GCGCATGCTGCGGCTGGGAGGTCGAGGAGTCTGACACAGGTGAACACAGAGCAGC 1249
 Db 793 GCGCATGCTGCGGCTGGGAGGTCGAGGAGTCTGACACAGGTGAACACAGAGCAGC 852
 Qy 1250 GTGAGGTGGTGTCTGTGTGCTGCTGCGTACGCGGCCACGCGCTCTTCAACTACAGC 1309
 Db 853 GTGAGGTGGTGTCTGTGTGCTGCTGCGTACGCGGCCACGCGCTCTTCAACTACAGC 912
 Qy 1310 ATCAGCAGGAGCTCTGCGCCAGGTGTGGTGGCGGAGGCTGCGTGAACCTCTGAC 1369
 Db 913 ATCAGCAGGAGCTCTGCGCCAGGTGTGGTGGCGGAGGCTGCGTGAACCTCTGAC 972
 Qy 1370 CTGGTTCATGGGCTGCGCGGATGCGCCAGATGGGCACTGGTCTTGGCTTCTCCAGAGG 1429
 Db 973 CTGGTTCATGGGCTGCGCGGATGCGCCAGATGGGCACTGGTCTTGGCTTCTCCAGAGG 1032
 Qy 1430 GGTGCCAGCTGACAGAGTTCCTCCAGTACGTGAAGACGACCTGCGCCCTGCGCACCCAG 1489
 Db 1033 GGTGCCAGCTGACAGAGTTCCTCCAGTACGTGAAGACGACCTGCGCCCTGCGCACCCAG 1092
 Qy 1490 CCGGCTTCTGCTCTGCGCCAGGTGTGGTGGCGGAGGAGGCTGCGAGGAGACCTGGTGGGC 1549
 Db 1093 CCGGCTTCTGCTCTGCGCCAGGTGTGGTGGCGGAGGAGGAGGCTGCGAGGAGACCTGGTGGGC 1152
 Qy 1550 CAGCGTGGCGGAGTGTGACTGATCATCGCTGACAGACGTGAGCGACAGGCTTAATAC 1609
 Db 1153 CAGCGTGGCGGAGTGTGACTGATCATCGCTGACAGACGTGAGCGACAGGCTTAATAC 1212
 Qy 1610 CACGACAGGTTCTTCTGACGAGCTGTATAGCGTGGCCCGGAGGCTGACACACT 1669
 Db 1213 CACGACAGGTTCTTCTGACGAGCTGTATAGCGTGGCCCGGAGGCTGACACACT 1272

Qy 1670 CTTTCACTGCAACGCTCCTCAGGCTGCCCGCGCAGAGACCCCTGTAAGCCCTGGCAGGTGAGC 1729
 Db 1273 CTTTCACTGCAACGCTCCTCAGGCTGCCCGCGCAGAGACCCCTGTAAGCCCTG 1322
 Qy 1730 CCGGAGATGGGGTGTGTGTCTGTGATGTGCCAGGCCACCGCAGGCCACCCAC 1789
 Db 1323 ----- 1322
 Qy 1790 GCCTGAGCTGGAGTGGCTGGCGCTCAGCCCGCTGCCCGCGCAGGCTCCTGAGAAC 1849
 Db 1323 ----- GCAGCTCCTGGAGAAC 1338
 Qy 1850 ATGTACAACCTGACCTTCCACGTGGCGGCTGCGCTGCGGTTCGACAGAGCGGAAAC 1909
 Db 1339 ATGTACAACCTGACCTTCCACGTGGCGGCTGCGCTGCGGTTCGACAGAGCGGAAAC 1398
 Qy 1910 GTGACATGAGTACGACCTGAAAGCTGTGGTGTGGCAGGCTCAGTGCACAGGCTCCAC 1969
 Db 1399 GTGACATGAGTACGACCTGAAAGCTGTGGTGTGGCAGGCTCAGTGCACAGGCTCCAC 1458
 Qy 1970 GACGTGGCGAGTTCAACGCGCAGCTCAGGACAGAGCGCTGAAAGATCCGCTGGCACAG 2029
 Db 1459 GACGTGGCGAGTTCAACGCGCAGCTCAGGACAGAGCGCTGAAAGATCCGCTGGCACAG 1518
 Qy 2030 TCTGACCAACCAAGTGTAGGTGAGGTGTGCCAGGCTGCCCGTGTAGCCCCCGCGG 2089
 Db 1519 TCTGACCAAC ----- 1527
 Qy 2090 CAGGCGCAGCTGGGGTGGGGCGCTTCCAGTCTCCGCTGGGCGATGCCAGCGAGCA 2149
 Db 1528 ----- 1527
 Qy 2150 GAGCCAGACCCAGGCTGTGCGCAGAGCCGCTGCCCGTGTCCGCGCAGTGCACAGG 2209
 Db 1528 ----- CAGAGCCCGTGTCCGATGTCTGCGCGCAGTGCACAGG 1564
 Qy 2210 AGGCGCAGGTGCGCGGCTCAAGGGTTCACCTCTGCTGTGCTACGACTGTGAGTCTCG 2269
 Db 1565 AGGCGCAGGTGCGCGGCTCAAGGGTTCACCTCTGCTGTGCTACGACTGTGAGTCTCG 1624
 Qy 2270 AGGCGGCGAGTACCGGCACAAACCCAGGTGAGCGCCCTTCCCGGCGAGCGGGTGGAA 2329
 Db 1625 AGGCGGCGAGTACCGGCACAAAC ----- 1648
 Qy 2330 CGCAGAGGCGAGGTCTCTGCAAGTCTGACTCTGAGACAGAGCCACAGGGTACAG 2389
 Db 1649 ----- 1648
 Qy 2390 ACGAACACCCAGCGCCCTTCTCTCAAGACGACATGCGCTGCGACCTTTTGTGGCC 2449
 Db 1649 ----- CAGACGACATGCGCTGCGACCTTTTGTGGCC 1678
 Qy 2450 AGGATGAGTGTCCCGGAGCGAAGCAGACGCTGCTCCGCGCAGGTCTCGGTTCCTGG 2509
 Db 1679 AGGATGAGTGTCCCGGAGCGAAGCAGACGCTGCTTCCGCGCAGGTCTCGGTTCCTGG 1738
 Qy 2510 CATGGGCGAGCGGCTGTGTGCTGTCTCTCTGCTGAGCTGCGCTGCGGCTTGG 2569
 Db 1739 CATGGGCGAGCGGCTGTGTGCTGTCTCTCTGCTGAGCTGCGGCTTGG 1798
 Qy 2570 TGCTGGCTTTTGGGCTGTTCCTTACCATCGGACAGCCCACTGTTTCAAGGCTCGG 2629
 Db 1799 TGCTGGCTTTTGGGCTGTTCCTTACCATCGGACAGCCCACTGTTTCAAGGCTCGG 1858
 Qy 2630 GGGGCGCTTGGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2689
 Db 1859 GGGGCGCTTGGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1918
 Qy 2690 TGTTCCTTGGCGCAGCCAGCCCTGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2749
 Db 1919 TGTTCCTTGGCGCAGCCAGCCCTGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1978

QY	2750	CGCTCACGGCTGCTGAGCACA	CTCTTCCTGCGAGGCGCCGAGATCTTCGTGAGTGAAG	2809
DB	1979	CGCTCACGGGCTGCGTGA	GCACATCTTCCTGCGAGGCGCGAGATCTTCGTGAGTGAAG	2038
QY	2810	AACTGCCCTCTGAGCTGGGCAGAC	CGGCTGAGTGGCTGCTCGCGGGGCGCCTGCGSCCTGGC	2869
DB	2039	AACTGCCCTCTGAGCTGGGCAGAC	CGGCTGAGTGGCTGCTCGCGGGGCGCCTGCGSCCTGGC	2098
QY	2870	TGTTGGTGTCTGTGGCCATG	CTGTGTGGAGTGGCACTGTGTCACTCTGTGTACCTGTGTGGCCT	2929
DB	2099	TGTTGGTGTCTGTGGCCATG	CTGTGTGGAGTGGCACTGTGTCACTCTGTGTACCTGTGTGGCCT	2158
QY	2930	TCCCGCCGGAGGTGTGACGAC	ATGGCACTGCTGTGCCACGGAGGCGCTGGTGCACGTGCC	2989
DB	2159	TCCCGCCGGAGGTGTGACGAC	ATGGCACTGCTGTGCCACGGAGGCGCTGGTGCACGTGCC	2218
QY	2990	GCACACGCTCTCTGGGTCA	GCTTCGGCCTTAGCGCACGCCACCAATGCCACGCTGGSCCTTTC	3049
DB	2219	GCACACGCTCTCTGGGTCA	GCTTCGGCCTTAGCGCACGCCACCAATGCCACGCTGGSCCTTTC	2278
QY	3050	TCTGCTTCTGTGGCACTTTC	CTGTGTGGAGCCAGCGCGGGCTGTCAACCGTGGCCCGTG	3109
DB	2279	TCTGCTTCTGTGGCACTTTC	CTGTGTGGAGCCAGCGCGGGCTGTCAACCGTGGCCCGTG	2338
QY	3110	GCCTCACCTTTGCCATGCT	GGCCTTCACTACCTGTGCTCTCTTTGTGCCCTCCCTGG	3169
DB	2339	GCCTCACCTTTGCCATGCT	GGCCTTCACTACCTGTGCTCTCTTTGTGCCCTCCCTGG	2398
QY	3170	CCAAATGTCAGGTGGTCTC	TACGGCCCGCGTGAGATGGGGCGCCCTCCTGCTCTGTGTCC	3229
DB	2399	CCAAATGTCAGGTGGTCTC	TACGGCCCGCGTGAGATGGGGCGCCCTCCTGCTCTGTGTCC	2458
QY	3230	TGGGCATCCTGGCTGGCTT	CCACCTGCCAGGTGTACCTGTCTATCGGGAGCAGAGGC	3289
DB	2459	TGGGCATCCTGGCTGGCTT	CCACCTGCCAGGTGTACCTGTCTATCGGGAGCAGAGGC	2518
QY	3290	TCAACACCCCCAGTTCTT	CTCTGGAGGGGGCCCTGGGGATGCCCAAGGCCAGAAATGACG	3349
DB	2519	TCAACACCCCCAGTTCTT	CTCTGGAGGGGGCCCTGGGGATGCCCAAGGCCAGAAATGACG	2578
QY	3350	GGAAACAGAGAAATCAGGG	AAACATCAGTGAACCCAACTGTGTATCTCAGCCCCCGGTGA	3409
DB	2579	GGAAACAGAGAAATCAGGG	AAACATCAGTGAACCCAACTGTGTATCTCAGCCCCCGGTGA	2638
QY	3410	ACCCAGACTTAGCTGGCAT	CCCCCCCCAAGCCAGCAATGACCCGTGTCTCGCTACAGAC	3469
DB	2639	ACCCAGACTTAGCTGGCAT	CCCCCCCCAAGCCAGCAATGACCCGTGTCTCGCTACAGAC	2698
QY	3470	CCTCCCGCTCTTAGTTCT	GTGACCCCGAGTTGTCTCTGACCTCAGCCCAACAGTGGACCCCT	3529
DB	2699	CCTCCCGCTCTTAGTTCT	GTGACCCCGAGTTGTCTCTGACCCCTCAGCCCAACAGTGGACCCCT	2758
QY	3530	AGGCCTGGAGACGTGGAC	ACCCCTGTGACCAATC	3563
DB	2759	AGGCCTGGAGACGTGGAC	ACCCCTGTGACCAATC	2792

RESULT 11

ADG19751
ID ADG19751 standard; cDNA; 3489 BP.
XX
XX AC ADG19751;
XX
XX DT 26-FEB-2004 (first entry)
XX
XX DE Human G protein coupled receptor (GPCR) 50289 cDNA.
XX
XX cytostatic; nephrotropic; antiinflammatory; cardiac; respiratory;
KW gastrointestinal; neuroprotective; angiogenesis stimulator; gene therapy;
KW 19636; 2466; 43238; 1983; 52881; 2396; 45449; 50289; 52872; 28908;
KW cellular proliferative disorder; brain disorder; renal disorder;
KW kidney disorder; inflammatory disorder; cardiovascular disorder;
KW liver disorder; intestinal disorder; respiratory disorder;
KW

KW	angiogenic disorder; human; G protein coupled receptor; GPCR; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	US2003215860-A1.
XX	
PD	20-NOV-2003.
XX	
PF	03-APR-2003; 2003US-00407079.
XX	
PR	29-FEB-2000; 2000US-0186059P.
PR	24-MAR-2000; 2000US-0191845P.
PR	22-MAY-2000; 2000US-0206019P.
PR	17-NOV-2000; 2000US-00715790.
PR	28-FEB-2001; 2000US-00796338.
PR	22-MAY-2001; 2001US-00863200.
PR	22-AUG-2001; 2001US-0314041P.
PR	22-AUG-2001; 2001US-0314185P.
PR	21-AUG-2002; 2002US-00225094.
PR	22-AUG-2002; 2002US-00226102.
PR	15-OCT-2002; 2002US-00272417.
PR	29-OCT-2002; 2002US-00282837.
XX	
PA	(MILL-) MILLENNIUM PHARM INC.
XX	
PI	Glucksmann MA, Silos-Santiago I, Carroll JM, Galvin KM;
XX	
DR	WPI; 2004-010777/01.
DR	P-PSDB; ADG19752.
XX	
PT	New nucleic acid or polypeptide 18636, 2466, 43238, 1983, 52881, 2398,
PT	45449, 50289, 52872 or 26908, useful in preparing a composition for
PT	treating e.g., cellular proliferative, brain, kidney, inflammatory or
PT	angiogenic disorder.
XX	
PS	Claim 2; SEQ ID NO 89; 163pp; English.
XX	
CC	The invention describes a new isolated 18636, 2466, 43238, 1983, 52881,
CC	2398, 45449, 50289, 52872 or 26908 nucleic acid molecule comprising: a
CC	sequence comprising 939-3489 bp or its fragment comprising at least 15
CC	nucleotides; a sequence encoding a polypeptide comprising a sequence
CC	having 223-952 amino acids, or its allelic variant or fragment comprising
CC	at least 15 contiguous amino acids; or a sequence that hybridises with
CC	(1) under stringent conditions. The nucleic acid or polypeptide is useful
CC	in preparing a composition for treating a disorder characterised by
CC	aberrant 18636, 2466, 43238, 1983, 52881, 2398, 45449, 50289, 52872 or
CC	26908 activity e.g., cellular proliferative, brain, renal, kidney,
CC	inflammatory, cardiovascular, liver, intestinal, respiratory or
CC	angiogenic disorder. This sequence encodes novel human protein 50289, a G
CC	protein coupled receptor (GPCR).
XX	
XX	Sequence 3489 BP; 578 A; 1189 C; 1102 G; 612 T; 0 U; 8 Other

Query Match	58.9%	Score 2099.2	DB 12	Length 3489
Best Local Similarity	81.6%	Pred. No. 0		
Matches 2769; Conservative	0	Mismatches	13	Indels 612; Gaps 5

Qy	170	GGGCGACGCACTGCCTGCTTGGAAAGTTCCTCTGCCATGCTGGGCCCTGCTGTCC	229
Db	11	GAGTCGACCACTGCGTCGCGCTGTTGGAAGTTGCCTCTGCCATGCTGGGCCCTGCTGTCC	70
Qy	230	TGGGCTCTAGCCTCTGGGCTCTCCCTGCACCTGGGACGGGGGCCCATTTGTCCTGTCA	289
Db	71	TGGGCTCTAGCCTCTGGGCTCTCCTGCACTCTGGACGGGGGCCCATTTGTCCTGTCA	130
Qy	290	AGCAACTTAGGATGAAGGGGGACTAGTGTCTGGGGGGGCTGTTCCCTCTGGCGAGGGCG	349
Db	131	AGCAACTTAGGATGAAGGGGGACTAGTGTCTGGGGGGGCTGTTCCCTCTGGCGAGGGCG	190
Qy	350	AGAGAGCTGGCTCCCGCAGCGGACACGGCCGACAGCCCTGTGTGCACCAAGTACAGAG	409
Db	191	AGAGAGCTGGCTCCCGCAGCGGACACGGCCGACAGCCCTGTGTGCA-----	238

QY 410 GTGGACGGCTGGGTGGGTGAGGTGACAGGTCTGGGTGCTCTGTGAGCTGGGGC 469
 Db 239 ----- 238
 QY 470 GAGGTGGCCATCTCGGTCTGTGTGGCCCGCAGGTCTCTCAAAACGGCCTGTCTGGGC 529
 Db 239 -----CCAGGTCTCTCTCAAAACGGCCTGTCTGGGC 269
 QY 530 ACTGGCCATGAATAATGGCCGTGGAGGATCAACAAAGTCGATCTGTGCTGCCGGCT 589
 Db 270 ACTGGCCATGAATAATGGCCGTGGAGGATCAACAAAGTCGATCTGTCTGCCGGCT 329
 QY 590 GCGCTGGGTACACCTCTTTGATACGTCTCGAGCTGTGTGGCCATGAAGCCGAG 649
 Db 330 GCGCTGGGTACACCTCTTTGATACGTCTCGAGCTGTGTGGCCATGAAGCCGAG 389
 QY 650 CCTCATGTTCTGGCCAAAGGAGGAGCGCGGACATCGCCGCTACTGTCAACTACGCA 709
 Db 390 CCTCATGTTCTGGCCAAAGGAGGAGCGCGGACATCGCCGCTACTGTCAACTACGCA 449
 QY 710 GTACAGCCCGGTGTGTGCTGTATCGGCGCCCACTCGTCAGAGCTCGCCATGCTAC 769
 Db 450 GTACAGCCCGGTGTGTGCTGTATCGGCGCCCACTCGTCAGAGCTCGCCATGCTAC 509
 QY 770 CGGCAAGTCTTCAAGTCTTCTCTCATGCCAGTGGGGCGCCGCCACCATCACCCACC 829
 Db 510 CGGCAAGTCTTCAAGTCTTCTCTCATGCC----- 540
 QY 830 CCCAACCAACCCCTGCCCGTGGGAGCCCTTGTGTAGAGAAATGTACATGACCCCA 889
 Db 541 ----- 540
 QY 890 CCCAGCCCTGCCCTGGGAGCCCTGTGTAGAGAAATGTCTTGGCCCTTCAGGTCTAC 949
 Db 541 -----CAGGTCTACGTAC 552
 QY 950 GTGTAGCATGGAGCTGTGAGCGCCCGGAGACTTCCCTCCTCTTCGCGACCCGT 1009
 Db 553 GTGTAGCATGGAGCTGTGAGCGCCCGGAGACTTCCCTCCTCTTCGCGACCCGT 612
 QY 1010 CCCAGCGACCTGTGAGTGAAGCGCGCGGAGCTGTGAGAGTTCGGTGGAAAC 1069
 Db 613 CCCAGCGACCTGTGAGTGAAGCGCGCGGAGCTGTGAGAGTTCGGTGGAAAC 672
 QY 1070 TGGGTGGCCGCTGGGAGCGACAGCATGATGCGCGGAGCTGTGAGAGTTCGGTGGAAAC 1129
 Db 673 TGGGTGGCCGCTGGGAGCGACAGCATGATGCGCGGAGCTGTGAGAGTTCGGTGGAAAC 732
 QY 1130 GCGCTGGCGCGGACGCGGACATCTGATCGCGGAGCTGTGAGAGTTCGGTGGAAAC 1189
 Db 733 GCGCTGGCGCGGACGCGGACATCTGATCGCGGAGCTGTGAGAGTTCGGTGGAAAC 792
 QY 1190 GCGGATGACTCGCGCTGGGAGGAGTGAAGAGCTGTGCAACAGTGAACAGAGGAGC 1249
 Db 793 GCGGATGACTCGCGCTGGGAGGAGTGAAGAGCTGTGCAACAGTGAACAGAGGAGC 852
 QY 1250 GTGCAAGTGTGCTGTCTGCTGCTGCGCGGAGCGCGGACGCGCTTCACTACAGC 1309
 Db 853 GTGCAAGTGTGCTGTCTGCTGCTGCGCGGAGCGCGGACGCGCTTCACTACAGC 912
 QY 1310 ATCAGCAGCAGGCTCTGCGCCAAAGTGTGGGTGGCGGAGGCTGTGAGCTCTGAC 1369
 Db 913 ATCAGCAGCAGGCTCTGCGCCAAAGTGTGGGTGGCGGAGGCTGTGAGCTCTGAC 972
 QY 1370 CTGGTCAATGGGCTGTGCGGAGTGAAGAGTGAAGAGCTGTGAGGCTGTGAGGCTGTGAGG 1429
 Db 973 CTGGTCAATGGGCTGTGCGGAGTGAAGAGTGAAGAGCTGTGAGGCTGTGAGGCTGTGAGG 1032
 QY 1430 GTTGGCCAGCTGACAGTTCCTCCAGTGTGAGTGAAGAGCTGTGAGGCTGTGAGGCTGTGAGG 1489
 Db 1033 GTTGGCCAGCTGACAGTTCCTCCAGTGTGAGTGAAGAGCTGTGAGGCTGTGAGGCTGTGAGG 1092
 QY 1490 CCGGCTTCTGCTCTGCTGGGCGAGAGGAGGAGGAGTCTGGAGGAGGAGCTGTGGGC 1549

1093 CCGGCTTCTGCTCTGCTGGCGAGAGGAGCAGGCTCTGGAGGAGGAGCTGTGGGC 1152
 QY 1550 CAGGCTGCGCGCAGTGTGACTCATCGCTGCAGAACTGAGCGAGGCTTAAATCAC 1609
 Db 1153 CAGGCTGCGCGCAGTGTGACTCATCGCTGCAGAACTGAGCGAGGCTTAAATCAC 1212
 QY 1610 CACAGACGTTCTGTCTACGAGCTGTGTATAGCTGGGCCAGGCTGTGCAACACT 1669
 Db 1213 CACAGACGTTCTGTCTACGAGCTGTGTATAGCTGGGCCAGGCTGTGCAACACT 1272
 QY 1670 CTTCACTGAACGCTCAGGCTGCGCGCAGAGAACCGCTGAAGCTGTGAGGCTGTGAGC 1729
 Db 1273 CTTCACTGAACGCTCAGGCTGCGCGCAGAGAACCGCTGAAGCTGTGAGGCTGTGAGC 1322
 QY 1730 CCGGAGATGGGGTGTGCTCTCTGCTGCTGCTGCCAGGCGCACGAGCGGCGCAC 1789
 Db 1323 ----- 1322
 QY 1790 GCCTGAGCTGAGGTGGCTGGCGCTCAGCCCGCTGCCCGCGAGCTCTGGAGAAC 1849
 Db 1323 -----GCAGCTCTGGAGAAC 1338
 QY 1850 ATGTACAACTGACCTTCCAGCTGGGGCGGCTGCGCTGCGGTTGCGAGCAGCGGAAAC 1909
 Db 1339 ATGTACAACTGACCTTCCAGCTGGGGCGGCTGCGCTGCGGTTGCGAGCAGCGGAAAC 1398
 QY 1910 GTGACATGAGTGAAGCTGAGCTGTGGTGTGGCAGGCTCAGTCCCGCAGGCTCCAC 1969
 Db 1399 GTGACATGAGTGAAGCTGAGCTGTGGTGTGGCAGGCTCAGTCCCGCAGGCTCCAC 1458
 QY 1970 GACGTGGCGAGCTTCAACGCGAGCTCAGGACAGAGCGCTGAAGATCCGTGGCACAG 2029
 Db 1459 GACGTGGCGAGCTTCAACGCGAGCTCAGGACAGAGCGCTGAAGATCCGTGGCACAG 1518
 QY 2030 TCTGACAACTGAGTGAAGTGGGTGGTGTGCCAGGCTGCGCGTGTAGCCCGCGG 2089
 Db 1519 TCTGACAACT----- 1527
 QY 2090 CAGGCGCAGCTTGGGGTGGGGCGGTTCCAGTCTCCGTGGGCTGCCAGCGGAGCA 2149
 Db 1528 ----- 1527
 QY 2150 CAGCAGACCCAGGCTGTGCGCAGAGAGCCGTGTCCCGTGTGCGCGAGTCCACAG 2209
 Db 1528 -----CAGAGCCGTGTCCCGTGTGCGCGAGTCCACAG 1564
 QY 2210 AGGCGCAGGTGCGCGGTTCAAGGGTTCCACTCTGCTGCTACGACTGTGAGTGTG 2269
 Db 1565 AGGCGCAGGTGCGCGGTTCAAGGGTTCCACTCTGCTGCTACGACTGTGAGTGTG 1624
 QY 2270 AGGCGCGAGCTTACCGGCAAAACCCAGGTGAGCGCGCTTCCCGCAGCGGGGTGGGAA 2329
 Db 1625 AGGCGCGAGCTTACCGGCAAAAC----- 1648
 QY 2330 CCGCAGCGGGAGGCTCTGCGCAAGTCTCTGAGCCAGAGCCACAGGCTACAG 2389
 Db 1649 ----- 1648
 QY 2390 AGGAAACCCAGCGCCCTTCTCTCTCAAGAGCATCGCTTGCACCTTTCTGGGC 2449
 Db 1649 -----CAGAGCATCGCTTGCACCTTTCTGGGC 1678
 QY 2450 AGGATGAGTGGTCCCGGAGCGAAGCAACAGTGTCTCCCGCGCAGGCTCTCGGTTCTTGG 2509
 Db 1679 AGGATGAGTGGTCCCGGAGCGAAGCAACAGTGTCTCCCGCGCAGGCTCTCGGTTCTTGG 1738
 QY 2510 CATGGCGCAGCGCTGTGCTGTCTGCTGTGCTGTGAGCTGTGAGCTGTGAGCTGTG 2569
 Db 1739 CATGGCGCAGCGCTGTGCTGTCTGCTGTGCTGTGAGCTGTGAGCTGTGAGCTGTG 1798
 QY 2570 TGCTGCTGCTTTGGGGCTGTGCTTCACTCGGAGCAGGCTGTGCTTCAAGGCTCGG 2629

XX

929

Qy	1231	CGAGGTGAAC	CAGAGCAGCGTGCAGTGTGCTGCTTCCGCTCCGTCGACGCCGCCCA	1299
Db	789	CCAGGTGAAC	CAGAGCAGCGTGCAGTGTGCTGCTTCCGCTCCGTCGACGCCGCCCA	848
Qy	1291	CGCCCTCTT	CAACTACAGATCAGCAGCAGGCTCTCGCCCAAGGTGTGGGTGCCCACGCA	1350
Db	849	CGCCCTCTT	CAACTACAGATCAGCAGCAGGCTCTCGCCCAAGGTGTGGGTGCCCACGCA	908
Qy	1351	GGCTGTGGT	GAACCTTGACCTTGACCTTGATGGGGCTGCCGGATGGCCAGATGGGCACGCT	1410
Db	909	GGCTGTGGT	GAACCTTGACCTTGACCTTGATGGGGCTGCCGGATGGCCAGATGGGCACGCT	968
Qy	1411	GCTTGGCTT	CCTCCAGAGGGGTGCCAGCTGCAGAGTTCCCCCAGTACCTGTAAGACGCA	1470
Db	969	GCTTGGCTT	CCTCCAGAGGGGTGCCAGCTGCAGAGTTCCCCCAGTACCTGTAAGACGCA	1028
Qy	1471	CTTGGCCCT	GGCCACCGACCGGCTTCTGTCTGTGCCCTGGGGCAGAGGAGCAGGGTCT	1530
Db	1029	CTTGGCCCT	GGCCACCGACCGGCTTCTGTCTGTGCCCTGGGGCAGAGGAGCAGGGTCT	1088
Qy	1531	GGAGGAGGA	CGTGTGGTGGCCACGCTGCCCGCAGTGTGATGTGCATCACGCTGCAGAACGT	1590
Db	1089	GGAGGAGGA	CGTGTGGTGGCCACGCTGCCCGCAGTGTGATGTGCATCACGCTGCAGAACGT	1148
Qy	1591	GAGCGCAGG	CTAAATCACCACAGACGTTCTCTGTCTAGCCAGCTGTGTATAGCGTGGC	1650
Db	1149	GAGCGCAGG	CTAAATCACCACAGACGTTCTCTGTCTAGCCAGCTGTGTATAGCGTGGC	1208
Qy	1651	CCAGGCCCT	GTGCAACAATCTTTAGTGCACCGCTCAGGCTGCCCGCGCAGGACCCCGT	1710
Db	1209	CCAGGCCCT	GTGCAACAATCTTTAGTGCACCGCTCAGGCTGCCCGCGCAGGACCCCGT	1268
Qy	1711	GAAGCCCT	GTGAGCCCGGAGATGGGGGTGTGCTGTCTCTGATGTGCCAGGC	1770
Db	1269	GAAGCCCT	GTGAGCCCGGAGATGGGGGTGTGCTGTCTCTGATGTGCCAGGC	1277
Qy	1771	CACCAGGCA	CGGCCACCAACGCTGAGCTGGAGTGGTGGCGGTCTCAGCCCCCGTCCC	1830
Db	1278	-----	-----	1277
Qy	1831	CCCGCAGCT	CTCTGGAGAACATGTATCAACCTGACCTTCCAGTGGCGGGGCTGCCGCTGCG	1890
Db	1278	---CGAGCTCTCTGGAGAACATGTATCAACCTGACCTTCCAGTGGCGGGGCTGCCGCTGCG	1334	
Qy	1891	GTTCGACAG	CAGCGAAACGTGGACATGAGCTAGCAGCTGAAGCTGTGGGTGTGGCAGGG	1950
Db	1335	GTTCGACAG	CAGCGAAACGTGGACATGAGCTAGCAGCTGAAGCTGTGGGTGTGGCAGGG	1399
Qy	1951	CTCAGTGC	CCAGGTTCCACGACGTGGGACAGTTTCAACGGCAGCTCTCAGGACAGAGCGCT	2010
Db	1395	CTCAGTGC	CCAGGTTCCACGACGTGGGACAGTTTCAACGGCAGCTCTCAGGACAGAGCGCT	1450
Qy	2011	GAAGATCC	CGCTGGCAGACGCTCTGACCAACCGTGAAGGTGAGGGTGGGTGTGCCAGCGTG	2070
Db	1455	GAAGATCC	CGCTGGCAGACGCTCTGACCAACCGTGTGACCAACAGGT	1480
Qy	2071	CCCGTGGT	AGCCCCCGCGCAGGCGCAGCCTTGGGGGTGGGGGCGCTTCCAGTCTCCCGT	2130
Db	1488	-----	-----	1488
Qy	2131	GGGCAATG	CCGACGAGCAGAGCCAGACCCAGGCTGTGCGCAGAGCCCGTGTCCCGG	2190
Db	1488	-----	-----GCCCGTGTCCCGG	1500
Qy	2191	TGCTCG	CGCAGTGCAGAGGGCCAGGTGCCCGGGTCAAGGGGTTCACCTCTCTGTGC	2250
Db	1501	TGCTCG	CGCAGTGCAGAGGGCCAGGTGCCCGGGTCAAGGGGTTCACCTCTCTGTGC	1560
Qy	2251	TAACGACT	GTGTGGAATGCGAGCGGGCAGCTACCGGCAAAACCCAGGTGAGCGCGCTTCC	2310
Db	1561	TAACGACT	GTGTGGAATGCGAGCGGGCAGCTACCGGCAAAACCCAGGTGAGCGCGCTTCC	1600

QY 2311 CGCAGGCGGGGTGGGAAACGACAGAGGGAGGGTCTCTGCCAAGTCTCTGACTCTGAGACC 2370
 Db 1604 ----- 1603
 QY 2371 AGAGCCACAGGGTACAGAGCAACACCCAGCCCTTCTCTCTCTACAGACGACATC 2430
 Db 1604 -----CAGACGACATC 1614
 QY 2431 GCCTGACACCTTTTGTGGCCAGGATGAGTGGTCCCGAGGAGGACACAGCTCTCTCCGC 2490
 Db 1615 GCTTGACACCTTTTGTGGCCAGGATGAGTGGTCCCGAGGAGGACACAGCTCTCTCCGC 1674
 QY 2491 CGCAGGTCTCGGTTCTCTGGCATGGGCGAGCCGCTGTGCTGTGCTGTCTCTCTCTGCTGCTG 2550
 Db 1675 CGCAGGTCTCGGTTCTCTGGCATGGGCGAGCCGCTGTGCTGTGCTGTCTCTCTCTGCTGCTG 1734
 QY 2551 AGCTGGCGTGGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 2610
 Db 1735 AGCTGGCGTGGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 1794
 QY 2611 CCACTGGTTTCCAGGCTTCCGCGGCGGCGGCTTGGGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 2670
 Db 1795 CCACTGGTTTCCAGGCTTCCGCGGCGGCGGCTTGGGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 1854
 QY 2671 GTCTGCTCAGGCTCTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTG 2730
 Db 1855 GTCTGCTCAGGCTCTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTG 1914
 QY 2731 CAGCCCTTGTCCACCTCCCGCTCAGGGGTGCTGTGAGACACTTCTCTGAGGGCGGC 2790
 Db 1915 CAGCCCTTGTCCACCTCCCGCTCAGGGGTGCTGTGAGACACTTCTCTGAGGGCGGC 1974
 QY 2791 GAGATCTTCTGTGAGTCAAGACTGCTCTGAGCTGGGCGAGCCGCTGAGTGGCTGCTGCTG 2850
 Db 1975 GAGATCTTCTGTGAGTCAAGACTGCTCTGAGCTGGGCGAGCCGCTGAGTGGCTGCTGCTG 2034
 QY 2851 CGGGGCGCTTGGGCTTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 2910
 Db 2035 CGGGGCGCTTGGGCTTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 2094
 QY 2911 ACTGTGACTGTGCTTCCCGCGGAGGTGTGACGCACTGGGCACTGTGCTGCCACG 2970
 Db 2095 ACTGTGACTGTGCTTCCCGCGGAGGTGTGACGCACTGGGCACTGTGCTGCCACG 2154
 QY 2971 GAGGCGCTGTGCTACGCGCACACGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2154
 Db 2155 GAGGCGCTGTGCTACGCGCACACGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2214
 QY 3031 AATGCCAGCTGGCTTCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3090
 Db 2215 AATGCCAGCTGGCTTCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2274
 QY 3091 TGCTACACGCTGCGTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3150
 Db 2275 CGCTACACGCTGCGTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2334
 QY 3151 TCTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3210
 Db 2335 TCTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2394
 QY 3211 GCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3270
 Db 2395 GCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2454
 QY 3271 CTCATGGGCGAGGCTTCAACACCGGAGTCTTCTGCTGAGGGGGCGCTTGGGAT 3330
 Db 2455 CTCATGGGCGAGGCTTCAACACCGGAGTCTTCTGCTGAGGGGGCGCTTGGGAT 2514
 QY 3331 GCCAAGGCGAGGCTTCAACACCGGAGTCTTCTGCTGAGGGGGCGCTTGGGAT 3390
 Db 2515 GCCAAGGCGAGGCTTCAACACCGGAGTCTTCTGCTGAGGGGGCGCTTGGGAT 2574
 QY 3391 GTGATCTAGCCCCGGTGAACCCAGACTTAGTGTGCGATCCCCCCCCCAAGCCAGCAATGACC 3450

Db 2575 GTGATCTAGCCCCGGTGAACCCAGACTTAGTGTGCGATCCCCCCCCAGCCAGCAATGACC 2634
 QY 3451 CGTGTCTCGCTACAGAGACCTCCCGCTCTAGGTTCTGACCCCGAGGTTGTCTCTGACCC 3510
 Db 2635 CGTGTCTCGCTACAGAGACCTCCCGCTCTAGGTTCTGACCCCGAGGTTGTCTCTGACCC 2694
 QY 3511 TGACCCCAAGTGGAGCCCTAGGCTGGAGCAGTGGACACCCCTGTGACCATC 3563
 Db 2695 TGACCCCAAGTGGAGCCCTAGGCTGGAGCAGTGGACACCCCTGTGACCATC 2747

RESULT 13
 AAL38462
 ID AAL38462 standard; cDNA; 3458 BP.
 XX
 AC AAL38462;
 XX
 DT 15-AUG-2002 (first entry)
 XX
 CD cDNA encoding a human G-protein coupled receptor (GPCR).
 XX
 KW G-protein coupled receptor; GPCR; gene chip; human; immune response;
 KW chromosomal position; transgenic animal; gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT CDS 30..2588
 FT /*tag= a
 FT /product= "Human G-protein coupled receptor"
 XX
 PN WO200230981-A1.
 XX
 PD 18-APR-2002.
 XX
 PF 13-MAR-2001; 2001WO-US007832.
 XX
 PR 10-OCT-2000; 2000US-00684393.
 XX
 PA (PEXE) PE CORP NY.
 XX
 PI Wei M, Zhong W, Ketchum KA, Difrancesco V, Beasley EM;
 XX
 DR WPI: 2002-444173/47.
 DR P-PSDB; AAO21501.
 XX
 PT Novel G protein coupled receptor, useful for raising antibodies, to
 PT elicit immune response, and as a reagent in assays designed to
 PT quantitatively determine levels of protein in biological samples.
 XX
 PS Claim 1; Fig 1; 82pp; English.
 XX
 CC The invention relates to an isolated G-protein coupled receptor (GPCR)
 CC polypeptide, comprising an 852 residue amino acid sequence, given in the
 CC specification, an allelic variant or ortholog of the protein, or a
 CC fragment comprising at least 10 contiguous amino acids of the protein.
 CC GPCR is useful for identifying a modulator of GPCR and an agent that
 CC binds to GPCR. GPCR and a gene chip comprising GPCR are useful as models
 CC for the development of human therapeutic agents. GPCR is useful for
 CC raising antibodies, to elicit immune response, as a reagent in assays
 CC designed to quantitatively determine levels of protein in biological
 CC samples, and as markers for tissues in which the corresponding protein is
 CC preferentially expressed. A gene chip containing GPCR is also useful as a
 CC probe for determining the chromosomal positions of nucleic acid molecules
 CC by means of in situ hybridisation, in making vectors containing the gene
 CC regulatory regions of a gene chip containing GPCR, for designing
 CC ribozymes, in making vectors that express GPCR, and for constructing host
 CC cells and transgenic animals expressing nucleic acid molecules and
 CC peptides. A host cell containing GPCR is useful for conducting cell-based
 CC assays involving GPCR protein or its fragments, and for identifying
 CC protein mutants in which these function is affected. The polynucleotide
 CC encoding GPCR can be used to treat disorders by gene therapy. This

1581 TGCTACGACTGTGTGACTGCGAGGCGGCGAGCTACCGGCAAAACC----- 1626
2308 TCCCGCAGCGCGGGGTGGGAACGACAGCAGGAGGGTCTGCGCAAGTCTGACTCTGAG 2367
1627 ----- 1626
2368 ACCAGAGCCACAGGGTACAAGACGAACACCCAGCGCCCTTCTCCTCTCTCACAGACGAC 2427
1627 -----CAGACGAC 1634
2428 ATGCGCTGACACCTTTTGTGCGCAGGATGAGTGTCTCCCGAGCGAAGCACACGCTGCTTC 2487
1635 ATCGCTCGACCTTTTGTGCGCAGGATGAGTGTCTCCCGAGCGAAGCACACGCTGCTTC 1694
2488 CGCGCAGAGTCTCGGTCTCTGGCATGGGCGAGCGGCTGTGCTGTCTGCTCTCTGCTG 2547
1695 CGCGCAGAGTCTCGGTCTCTGGCATGGGCGAGCGGCTGTGCTGTCTGCTCTCTGCTG 1754
2548 CTGAGCCTCGCGCTGGGCTTGTGCTGGCTGTGCTTTGGGGCTGTTCCTTACCATCGGGAC 2607
1755 CTGAGCCTCGCGCTGGGCTTGTGCTGGCTGTGCTTTGGGGCTGTTCCTTACCATCGGGAC 1814
2608 AGCCCACTGCTTACAGCCTCGGGGGGGCCCCCTGCTGCTTTTGCCCTGTGTGCTGGGC 2667
1815 AGCCCACTGCTTACAGCCTCGGGGGGGCCCCCTGCTGCTTTTGCCCTGTGTGCTGGGC 1874
2668 CTGGTCTGCTGAGCTGCTCTCTGCTTCCCTGGCGAGCGCCAGCCCTGCGGATGCTGGCC 2727
1875 CTGGTCTGCTGAGCTGCTCTCTGCTTCCCTGGCGAGCGCCAGCCCTGCGGATGCTGGCC 1934
2728 CAGCAGCCTTGTCCACCTCCCGCTCACGGGCTGCTGAGCAGCACTTCTCTGAGGGCG 2787
1935 CAGCAGCCTTGTCCACCTCCCGCTCACGGGCTGCTGAGCAGCACTTCTCTGAGGGCG 1994
2788 GCCAGACTTCTGTGAGTGCAGAACTGCTCTGAGCTGGGCAGACCGGCTGAGTGGCTGC 2847
1995 GCCAGACTTCTGTGAGTGCAGAACTGCTCTGAGCTGGGCAGACCGGCTGAGTGGCTGC 2054
2848 CTGCGGGGGCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 2907
2055 CTGCGGGGGCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 2114
2908 TGCACCTGTGTACCTGTGTGGCTTTCCCGCGAGTGTGTGACGACTGCGACATGCTGCC 2967
2115 TGCACCTGTGTACCTGTGTGGCTTTCCCGCGAGTGTGTGACGACTGCGACATGCTGCC 2174
2968 ACGAGGCGCTGTGTGCACTGCCGACACAGCTCTCTGGGTGAGCTTTCGGCTTACGCGCGCC 3027
2175 ACGAGGCGCTGTGTGCACTGCCGACACAGCTCTCTGGGTGAGCTTTCGGCTTACGCGCGCC 2234
3028 ACCAATGCACGCTGGCTTCTGCTTCTGCTGGGCACTTCTGCTGGGAGCGGCGCGCG 3087
2235 ACCAATGCACGCTGGCTTCTGCTTCTGCTGGGCACTTCTGCTGGGAGCGGCGCGCG 2294
3088 GGCTGTACAAACGCTGGCTTCTGCTTTCGCACTGCTGGCTTCTGCTTCTGCTTCTGCTGG 3147
2295 GGCGCTACAAACGCTGGCTTCTGCTTTCGCACTGCTGGCTTCTGCTTCTGCTTCTGCTGG 2354
3148 GTCTCTTGTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 3207
2355 GTCTCTTGTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 2414
3208 GGCGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 3267
2415 GGCGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 2474
3268 CTGCTCATGCGGAGCGGCTCAACACCGCGAGTCTTCTGCTGGAGGGGCGCTGGG 3327
2475 CTGCTCATGCGGAGCGGCTCAACACCGCGAGTCTTCTGCTGGAGGGGCGCTGGG 2534
3328 GATGCCCAAGGCCAGAAATGACGGGAACACAGGAATCAGGGGAACATGAGTGACCCCAAC 3387

2535 GATGCCCAAGGCCAGAAATGACGGGAACACAGGAATCAGGGGAACATGAGTGACCCAAC 2594
3388 CTGTGATCTCAGCCCCGGTGAACCCAGACTTAGCTGCGATCCCCCCCAAGCCAGCAATG 3447
2595 CTGTGATCTCAGCCCCGGTGAACCCAGACTTAGCTGCGATCCCCCCCAAGCCAGCAATG 2654
3448 ACCCGTGTCTCGCTACAGAGACCCCTCCCGCTCTAGGTTCTGACCCCGAGGTTGTCTCTGA 3507
2655 ACCCGTGTCTCGCTACAGAGACCCCTCCCGCTCTAGGTTCTGACCCCGAGGTTGTCTCTGA 2714
3508 CCTGACCCCAAGTGAAGCCCTAGGCTGGAGCAGCTGGACACCCCTGTGACCATC 3563
2715 CCTGACCCCAAGTGAAGCCCTAGGCTGGAGCAGCTGGAGCAGCCCTGTGACCATC 2770

RESULT 14
ACA62666
ID ACA62666 standard; cDNA; 3458 BP.
XX ACA62666;
XX AC
XX 19-AUG-2003 (first entry)
XX cDNA encoding human calcium sensing G-protein coupled receptor.
XX Human; ss; gene; GPCR; G-protein coupled receptor; gene therapy;
XX Parkinson's disease; Huntington's disease; Tourette's syndrome.
XX Homo sapiens.
XX Key
XX CDS 30..2588
XX Location/Qualifiers
XX /*tag= a
XX /product= "G-protein coupled receptor"

US2003036089-A1.
XX
XX
XX 20-FEB-2003.
XX
XX 02-OCT-2002; 2002US-00261482.
XX
XX 20-DEC-1999; 99US-0172600P.
XX 10-OCT-2000; 2000US-00684393.
XX (APPL-) APPLERA CORP.
XX
XX
XX Wei M, Zhong W, Ketchum XA, Di Francesco V, Beasley EM;
XX WPI; 2003-492117/46.
XX P-PSDB; ABU62106.
XX
XX New isolated human G-protein coupled receptor proteins, useful for
XX treating e.g. Parkinson's disease, Huntington's disease or Tourette's
XX syndrome, or for developing human therapeutics and diagnostic
XX compositions.
XX
XX Claim 4; Fig 1A; 46pp; English.
XX
XX The invention relates to an isolated human G-protein coupled receptor
XX (GPCR) peptide. The human GPCR peptides and nucleic acid molecules are
XX useful in the development of human therapeutics and diagnostic
XX compositions. The peptides are useful for treating disorders (e.g.
XX Parkinson's disease, Huntington's disease or Tourette's syndrome).
XX characterised by an absence of, inappropriate, or unwanted expression of
XX the GPCR protein, or disorders mediated by proteases. These molecules are
XX particularly useful as models for developing human therapeutic targets,
XX identifying therapeutic proteins, or serving as targets for the
XX development of human therapeutic agents that modulate GPCR activity in
XX cells and tissues that express the GPCR. The peptides are also useful for
XX raising antibodies or eliciting an immune response, as a reagent
XX (including the labelled reagent) in assays designed to quantitatively
XX determine levels of the protein (or its binding partner or ligand) in
XX biological fluids, or as markers for tissues in which the corresponding

CC protein is preferentially expressed. The agents identified are useful for
CC treating a subject with a disorder mediated by human proteases. The
CC present sequence represents cDNA encoding human calcium sensing G-protein
CC coupled receptor

SQ Sequence 3458 BP; 590 A; 1179 C; 1092 G; 597 T; 0 U; 0 Other;

Query Match 58.4%; Score 2080.4; DB 9; Length 3458;

Best Local Similarity 81.7%; Pred. No. 0;
Matches 2743; Conservative 0; Mismatches 1; Indels 612; Gaps 5;

208 GCCATGCTGGGCCCTGCTGTCTCTGGGCTCAGCCTCTGGGCTCTCTGCACCTGGGACG 267

27 GCCATGCTGGGCCCTGCTGTCTGGGCCTCAGCCCTCTGGGCTCTCCTGCACCTGGGACG 86

268 GGGGCCCCATTGTG CCTGTCA CAGCAACTTAGGATGAAGGGGGACTACGTGCTGGGGGGG 327

b 87 GGGGCCCAATTGTGCTGTCA CAGCAACTTAGGATGAAGGGGGGACTACGTGCTGGGGGG 146

328 CTGTTCCCCCTGGGCGAGGCCGAGGAGGCTGGCCTCCGACCGGACACGGCCACGACG 387

b
147 CTGTTCCCTGGGGCGAGGCCTGGCTCCCCCGACCGCAGC

[illegible][illegible]

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200 AGTCCGATCTGCTGCCCCGGCTGCGCTACGACCTCTTGGATACGCTGCTCGAGT 343

628 CAGGGGGCAAGAGCCACGCCCATGTTCCCTGGCCAAAGGCAGGCAGCCGACATCG 687

346 C G G G G G C C A I G A A G C C C A G C C T C A T G T T C C T G G C C A A G G C A G G C G C G A C A T C G 405

688 CCGCCCTACCTGCAACATACACGCAGTACCAGGCCCGTGGCTGTCACTGGGGCCCACT /47

406 CCGCC¹AC¹GC¹AACTACACGCAGTACCAGCCCCG¹TGTGGCTGT¹CATCGGGCCCCACT 465

CGTCAGAGCTCGCCATGGTCAACGGCAAGTTCTTCAGCTTCTTCTCCTCATGCCCCAGTGGG 807

CGTCAGAGCTCGCCATGGTCAACGGCAAGTTCTTCAGCTTCTTCCTCATGCC-- 518

808 GCGCCCCCACCATCACCCACCCCCAACCAACCCCTGCCCGCTGGGAGCCCCCTTGTGTCA 867

519 ----- 518

868 GGAGATGCTACATGCACCCACCCAGCCCTGCCCTGGAGCCCTGTGTGTCAGAAATGCT 927

519 ----- 518

928 CTTGGCCTTGCAGGTCAGCTACGGTGCTAGCATGGAGCTGCTAGCGCCCGGAGACCTT 987

519 -----CAGGTCACTACGGTGCTAGCATGGAGCTGCTAGCGCCCGGAGACCTT 568

988 CCCCTCCTTCTTCCGCACCGTGCCAGCGACCGTGTGCAGCTGACGGCCGCCGGAGCT 1047

b 569 CCCCTCCTTCTTCCGCACCGTGCCCAAGCACCGTGTCAGCTGACGGCCGCCGCGAGCT 628

1048 GCTGCAGGAGTTCGGCTGGAAGTGGTGGCCGCCCTGGCAGCGACGAGTACGGCCG 1107

b 629 GCTGCAGGAGTTCGGCTGGAAGTGGTGGCCGCCCTGGCAGCAGCAGTACGGCCG 688

1108 GCAGGGCCTGAGCATCTTCTCGGCCCTGGCCGGCACGCGGCATCTGCATCGGCACGA 1167

Db	689	GCAGGGCCTGAGCATCTTTCTGGCCCTTGGCCCGCGGCACGCGGGCATCTGATCGCGCACGA	748
Qy	1168	GGCCCTGGTGCCCGCTGCCCGCTGCCGATGACTCGCGCTGGGGAAGGTGACGACGCTCCT	1227
Db	749	GGCCCTGGTGCCCGCTGCCCGCTGCCGATGACTCGCGCTGGGGAAGGTGACGACGCTCCT	808
Qy	1228	GCACCAAGGTGAACCAAGACAGCGGTGACGTGGTGCTGTCTGTTCGCTTCCGTGCAAGCCGC	1287
Db	809	GCACCAAGGTGAACCAAGACAGCGGTGACGTGGTGCTGTCTGTTCGCTTCCGTGCAAGCCGC	868
Qy	1288	CCACGCGCCTCTTCAACTACAGATCAGCAGCAGGCTCTCGCCCAAGGCTGGGTGGCCAG	1347
Db	869	CCACGCGCCTCTTCAACTACAGATCAGCAGCAGGCTCTCGCCCAAGGCTGGGTGGCCAG	928
Qy	1348	CGAGGCTGGCTGACCTCTGCACTGTGTCAATGGGGCTGCCCCGGAATGGCCAGATGGGCA	1407
Db	929	CGAGGCTGGCTGACCTCTGCACTGTGTCAATGGGGCTGCCCCGGAATGGCCAGATGGGCA	988
Qy	1408	GGTGCTTGGCTTCCCTCCAGAGGGTGCCCAAGCTGACAGAGTTTCCCCAGTACGCTGAAGAC	1467
Db	989	GGTGCTTGGCTTCCCTCCAGAGGGTGCCCAAGCTGACAGAGTTTCCCCAGTACGCTGAAGAC	1048
Qy	1468	GCACCTGGCCCTGGCCACCGACCCCGCCTTCTGCTGCGCTGGCGAGAGGAGCAGGG	1527
Db	1049	GCACCTGGCCCTGGCCACCGACCCCGCCTTCTGCTGCGCTGGCGAGAGGAGCAGGG	1108
Qy	1528	TCTGGAGGAGGACGTGGTGGGCCAGCGCTGCCCGAGTGTGACTGCATCAGCGTCAGAA	1587
Db	1109	TCTGGAGGAGGACGTGGTGGGCCAGCGCTGCCCGAGTGTGACTGCATCAGCGTCAGAA	1168
Qy	1588	CGTGAGCGAGGGCTAAATCACACACAGAGCTTCTGTCTACGAGCTGTGTATAGCGT	1647
Db	1169	CGTGAGCGAGGGCTAAATCACACACAGAGCTTCTGTCTACGAGCTGTGTATAGCGT	1228
Qy	1648	GGCCCAAGCCCTGCACAACTCTTCAGTGCAACGCCTCAGGCTGCCCGCGGAGAGCC	1707
Db	1229	GGCCCAAGCCCTGCACAACTCTTCAGTGCAACGCCTCAGGCTGCCCGCGGAGAGCC	1288
Qy	1708	CGTGAAGCCCTGCAGGTGAGCCCGGAGATGGGGTGCTGTCTCTCTGATGATGCCCA	1767
Db	1289	CGTGAAGCCCTG	1300
Qy	1768	GGCCACAGGACCGGCCACACGCTGAGCTGGAAGTGCTGGCGGCTCAGCCCGCTCC	1827
Db	1301	-----	1300
Qy	1828	CCGCCCGAGCTCTGGGAACATGTACAACTGACCTTCCAGCTGGCGGGCTCGCGT	1887
Db	1301	-----GCAGCTCTGGGAACATGTACAACTGACCTTCCAGCTGGCGGGCTCGCGT	1354
Qy	1888	CGCGTTTCGACAGCAGCGGAAAAGTGGACATGGAGTACGACCTGAAGCTGTGGGTGTGGCA	1947
Db	1355	CGCGTTTCGACAGCAGCGGAAAAGTGGACATGGAGTACGACCTGAAGCTGTGGGTGTGGCA	1414
Qy	1948	GGGCTCAGTGCCAGGCTCCAGCTGGGCAAGCTTCAACGGCAGGCTCAGGACAGAGG	2007
Db	1415	GGGCTCAGTGCCAGGCTCCAGCTGGGCAAGCTTCAACGGCAGGCTCAGGACAGAGG	1474
Qy	2008	CTTGAAGATCCGCTGCGCACACGCTTCACAAACAGGCTGAGGTGAGGTGGGTGCCAGGC	2067
Db	1475	CTTGAAGATCCGCTGCGCACACGCTTCACAAAC	1505
Qy	2068	GTGCCCGTGGTAGCCCCCGCGGACGCTGGGGTGCGGCGCTGTCCAGTCTCC	2127
Db	1506	-----	1505
Qy	2128	CGTGGGCATGCCCGCAGAGAGAGCCAGACCCAGGCTGTGTGCGCAGAAGCCGCTGCC	2187
Db	1506	-----CAGAAAGCCGCTGTCC	1520
Qy	2188	CGTGCTCGCGCAGTGCCAGAGAGGCCAGGTGCGCCCGGTCAAGGGGTTCACCTCCTGC	2247
Db	1521	CGTGCTCGCGCAGTGCCAGAGAGGCCAGGTGCGCCCGGTCAAGGGGTTCACCTCCTGC	1580

QY	3328	GATGCCAAGCCCAAGATGACGGGAAACACAGGAAATCAGGGGAAACATGAGTGACCCCAAC	3387
DB	2535	GATGCCAAGCCCAAGATGACGGGAAACACAGGAAATCAGGGGAAACATGAGTGACCCCAAC	2594
QY	3388	CCTGTGATCTCAGCCCGGTTGACCCAGACTTAGCTGGATCCCGCCCAAGCCAGCAATG	3447
DB	2595	CCTGTGATCTCAGCCCGGTTGACCCAGACTTAGCTGGATCCCGCCCAAGCCAGCAATG	2654
QY	3448	ACCCTGTCTCGCTACAGAGACCCCTCCCGTCTAGGTTCTTAGCCCAAGGTTGTCCTCTGA	3507
DB	2655	ACCCTGTCTCGCTACAGAGACCCCTCCCGTCTAGGTTCTTAGCCCAAGGTTGTCCTCTGA	2714
QY	3508	CCCTGACCCCACTGAGCCCTAGGCTGGAGCAGCTGGACACCCCTGTGACCATC	3563
DB	2715	CCCTGACCCCACTGAGCCCTAGGCTGGAGCAGCTGGACACCCCTGTGACCATC	2770
RESULT 15			
ID	ABL55952	standard; cDNA; 2729 BP.	
XX	AC	ABL55952;	
XX	AC	(first entry)	
DT	17-JUN-2002	Human G-protein coupled receptor encoding cDNA SEQ ID NO 12.	
XX	XX	Human; GPCR; G-protein coupled receptor; receptor; anti-HIV; antitumour;	
KW	KW	antiinflammatory; antiallergic; antianaemic; antiasthmatic; virucide;	
KW	KW	immunosuppressive; dermatological; nephrotropic; antigout; antithyroid;	
KW	KW	cytostatic; neuroprotective; osteopathic; antipsoriatic; antirheumatic;	
KW	KW	antiarthritic; thymometric; antitumor; ophthalmological; antibacterial;	
KW	KW	fungicide; antiparasitic; protozoacide; antihelminthic; antidiabetic;	
KW	KW	antiarteriosclerotic; hepatotropic; anticonvulsant; anorectic; metabolic;	
KW	KW	antienetic; anti diarrhoeic; neuroleptic; cerebroprotective; nootropic;	
KW	KW	antiparkinsonian; depilatory; tranquilizer; hypotensive; vasotropic;	
KW	KW	cardiant; antianigral; vulnery; proliferative disorder; cancer;	
KW	KW	neurological disorder; Alzheimer's disease; Huntington's disease;	
KW	KW	Parkinson's disease; multiple sclerosis; meningitis; prion;	
KW	KW	cardiovascular disorder; acquired immunodeficiency syndrome; AIDS;	
KW	KW	Crohn's disease; diabetes mellitus; rheumatoid arthritis; gene; ss.	
XX	OS	Homo sapiens.	
XX	XX	Key Location/Qualifiers	
FH	FT	1..2592	
FT	FT	/*tag= a	
FT	FT	/product= "G-protein coupled receptor"	
XX	XX	W0200198323-A2.	
FN	XX	27-DEC-2001.	
PD	XX	15-JUN-2001; 2001WO-US019354.	
PF	XX	16-JUN-2000; 2000US-0212483P.	
PR	XX	23-JUN-2000; 2000US-0213950P.	
PR	XX	26-JUN-2000; 2000US-0214062P.	
PR	XX	07-JUL-2000; 2000US-0216595P.	
PR	XX	14-JUL-2000; 2000US-0218936P.	
PR	XX	19-JUL-2000; 2000US-0219154P.	
XX	PA	(INCY-) INCYTE GENOMICS INC.	
XX	XX	Lal P, Graul R, Hafalia AJA, Wallia NK, Thornton M, Nguyen DB;	
PI	PI	Lu Y, Gandhi AR, Patterson C, Kallilick DA, Baughn MR, Ramkumar J;	
PI	PI	Tribouley CM, Lee EA, Ding L, Burford N, Yao MG, Yang J;	
PI	PI	Griffin JA;	
XX	XX	WPI; 2002-139780/18.	
DR	DR	P-PSDB; ABB77318.	
XX	XX	Novel G-protein coupled receptor protein and polynucleotides useful for	

PT diagnosing, treating or preventing disorders of cell proliferation e.g.
 PT cancer, neurological and genetic disorder e.g. thalassemia.
 XX
 PS
 XX

Claim 48; Page 116-117; 121pp; English.

The invention relates to a G-protein coupled receptor protein (GCREC) polypeptide (ABB77317-ABB77326). The GCREC is useful for screening an agonist/antagonist of GCREC, a compound that specifically binds to GCREC or that modulates the activity of GCREC. GCREC is also useful as an immunogen for preparing antibodies which are useful for diagnosing a condition of disease associated with expression of GCREC in a subject, for detecting and purifying GCREC from a sample. The GCREC encoding polynucleotide (ABL55951-ABL55960) is useful for screening for a compound effective in altering expression of GCREC. GCREC is also useful for assessing toxicity of a test compound useful for treating a disease or condition associated with decreased expression or overexpression of functional GCREC. Examples of disorders include cell proliferative disorder such as arteriosclerosis, atherosclerosis, hepatitis, mixed connective tissue disease (MCTD), psoriasis and cancer including adenocarcinoma, leukaemia; a neurological disorder such as epilepsy, stroke, Alzheimer's disease, Huntington's disease, dementia, Parkinson's disease, retinitis pigmentosa, multiple sclerosis, bacterial and viral meningitis, abscess, subdural empyema; prion disease including kuru, Creutzfeldt-Jakob disease; fatal familial insomnia, neurofibromatosis, tuberous sclerosis, cerebral palsy, polymyositis; inherited, metabolic, endocrine, and toxic myopathies; myasthenia gravis, periodic paralysis; mental disorders including mood, anxiety, and schizophrenic disorders; seasonal affective disorder (SAD); akathisia, amnesia, catatonias, Tourette's disorder; tardive dyskinesia, dystonias, paranoid psychoses, vasculitis, cardiovascular disorders such as hypertension, congestive heart failure, ischemic heart disease, myocardial infarction, calcific aortic valve stenosis, infective endocarditis, endocarditis of systemic lupus erythematosus, cardiac transplantation; gastrointestinal disorder such as dysphagia, gastritis, anorexia, nausea, emesis, abdominal angina, infections of the intestinal tract, peptic ulcer, hepatitis, cirrhosis, diarrhoea, acquired immunodeficiency syndrome (AIDS), enteropathy, jaundice, Reye's syndrome, liver infarction; an autoimmune/inflammatory disorder such as AIDS, Addison's disease, adult respiratory distress syndrome, allergies, amyloidosis, anaemia, aschma, atherosclerosis, autoimmune thyroiditis, bronchitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoporosis, psoriasis, rheumatoid arthritis, scleroderma, Sjogren's syndrome, systemic lupus erythematosus, uveitis, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a metabolic disorders such as diabetes, obesity, and osteoporosis. The GCREC encoding polynucleotide is useful for gene therapy and for creating knock in humanised animals (pigs) or transgenic animals (mice or rats) to model human disease

Sequence 2729 BP; 413 A; 934 C; 879 G; 503 T; 0 U; 0 Other;

Query Match 58.4%; Score 2080; DB 6; Length 2729;
 Best Local Similarity 82.3%; Pred. No. 0;
 Matches 2723; Conservative 0; Mismatches 5; Indels 580; Gaps 6;

211 ATGCTGGGCGCTGCTGCTGGGCTCAGCCTTGGGCTCTCTGACACCTGGAGCGGG 270
 1 ATGCTGGGCGCTGCTGCTGGGCTCAGCCTTGGGCTCTCTGACACCTGGAGCGGG 60
 271 GCCCATTTGCTGTGCAGCAACTTAGGATGAAGGGGACTTACCTGCTGGGGGGCTG 330
 61 GCCCATTTGCTGTGCAGCAACTTAGGATGAAGGGGACTTACCTGCTGGGGGGCTG 120
 331 TTCCCTTGGGCGAGCCGAGGAGGTGGCTTCCGAGCGCGGACACGCGCCAGACGCT 390
 121 TTCCCTTGGGCGAGCCGAGGAGGTGGCTTCCGAGCGCGGACACGCGCCAGACGCT 180
 391 GTGTGACACGAGGTACAGAGTGGGACGGCTGGGTGGGTGAGGTGACGAGTCTGGG 450
 181 GTGTGCA----- 187

451 GTGCTCTGAGCTGGGGCCGAGGTGGCCATCTGCGGTTCTGTGTGGGCCCCAGGTTCTCT 510
 188 -----CCAGGTTCTCT 199
 511 CAACGGCCTGCTCTGGGCACTGGCCATGAAATGGCGGTGGAGAGATCAACAACAGT 570
 200 CAACGGCCTGCTCTGGGCACTGGCCATGAAATGGCGGTGGAGAGATCAACAACAGT 259
 571 CGGATCTGCTGCGCGGCTGGGCTTACGACCTCTTTGATACGTTGCTCGGAGCTG 630
 260 CGGATCTGCTGCGCGGCTGGGCTTACGACCTCTTTGATACGTTGCTCGGAGCTG 319
 631 TGGTGGCCATGAAGCCAGCCTCATGTTCTGGCCAGGAGGAGGCGGACATCGCG 690
 320 TGGTGGCCATGAAGCCAGCCTCATGTTCTGGCCAGGAGGAGGCGGACATCGCG 379
 691 CTTACTGCACTACACGAGTACACGCGGCTGGGCTGCTGCTGCTGCTGCTGCTGCT 750
 380 CTTACTGCACTACACGAGTACACGCGGCTGGGCTGCTGCTGCTGCTGCTGCTGCT 439
 751 CAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 810
 440 CAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 489
 811 CCCCCCATACACCCACCCCAACCCCTGCGGAGGAGGAGGAGGAGGAGGAGGAGG 870
 490 ----- 489
 871 GAATGCTACATGACCCCAACCCAGCCCTGCTGGAGCCCTGTGTGACAGAGATGCTCT 930
 490 ----- 489
 931 GGCCTTGCAGGTACGTACGTTAGTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAG 990
 490 -----CAGTACGTACGTTAGTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAG 542
 991 CTCCTTCTGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1050
 543 CTCCTTCTGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
 1051 GCAGAGTTCGGTGGAACTGGTGGCGCCCTGGGAGGAGGAGGAGGAGGAGGAGGAGG 1110
 603 GCAGAGTTCGGTGGAACTGGTGGCGCCCTGGGAGGAGGAGGAGGAGGAGGAGGAGG 662
 1111 GGGCTTGCAGTCTTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1170
 663 GGGCTTGCAGTCTTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 722
 1171 CTTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1230
 723 CTTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 782
 1231 CCAGTGTGAACAGAGCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1290
 783 CCAGTGTGAACAGAGCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 842
 1291 CGCCCTCTTCAACTACAGCATCAGCAGCAGGCTCTGCGCCAAAGGTGTGGTGGCCAGCA 1350
 843 CGCCCTCTTCAACTACAGCATCAGCAGCAGGCTCTGCGCCAAAGGTGTGGTGGCCAGCA 902
 1351 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1410
 903 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 962
 1411 GCTTGGCTTCTCCAGAGGGGTGCCAGCTGACAGTGTCCCGCCAGTACCTGAAGACGCA 1470
 963 GCTTGGCTTCTCCAGAGGGGTGCCAGCTGACAGTGTCCCGCCAGTACCTGAAGACGCA 1022
 1471 CTTGGCCCTTGGCCACCGACCCCGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1530
 1023 CTTGGCCCTTGGCCACCGACCCCGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1082
 1531 GGAGGAGGAGGCTGGTGGGCGGCGCTGCGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 1590

Db 1083 GGAGGAGCAGTGTGGCCAGCGCTGCCCGAGTGTGACTCATCGCTGCAGAACGT 1142
Qy 1591 GAGCGAGGGCTAAATCACCACAGAGCTTCTCTGTCTACGACGTGTGTATAGCTGGC 1650
Db 1143 GAGCGAGGGCTAAATCACCACAGAGCTTCTCTGTCTACGACGTGTGTATAGCTGGC 1202
Qy 1651 CCAGGCCCTGCACAACTCTTTCAGTGCAACCGCTCAGGCTGCCCGCGAGGACCCCGT 1710
Db 1203 CCAGGCCCTGCACAACTCTTTCAGTGCAACCGCTCAGGCTGCCCGCGAGGACCCCGT 1262
Qy 1711 GAAGCCCTGGCAGGTGAGCCCGGAGATGGGGGTGTGCTCTCTGTGATGTGCCAGGC 1770
Db 1263 GAAGCCCTG----- 1271
Qy 1771 CACGAGGACGGCCACACCGCTGAGCTGGAGTGGCTGGCGGCTCAGCCCGTCCCCG 1830
Db 1272 ----- 1271
Qy 1831 CCGCAGCTCCTGGAGAACATGTACAACTGACCTTCCACGTGGCGGGCTGCCGCTGCG 1890
Db 1272 ---GCAGCTCCTGGAGAACATGTACAACTGACCTTCCACGTGGCGGGCTGCCGCTGCG 1328
Qy 1891 GTTCGACAGCAGCGGAAACGTGGACATGGAGTACGACCTGAAGCTGTGGGTGTGGCAGGG 1950
Db 1329 GTTCGACAGCAGCGGAAACGTGGACATGGAGTACGACCTGAAGCTGTGGGTGTGGCAGGG 1388
Qy 1951 CTCAGTCCCGAGGCTCCACAGCGTGGCAGGTTCAACGGCAGGCTCAGGACAGAGCGCT 2010
Db 1389 CTCAGTCCCGAGGCTCCACAGCGTGGCAGGTTCAACGGCAGGCTCAGGACAGAGCGCT 1448
Qy 2011 GAAGATCCGCTGGCACACGCTGTGACAAACAGGTGAGGTGAGGGTGGGTGTGCCAGGGGTG 2070
Db 1449 GAAGATCCGCTGGCACACGCTGTGACAA----- 1475
Qy 2071 CCCGTGTAGCCCCCGCGCAGGCGCAGCTGTGGGGTGGGGGCGGTTCAGTCTCCGCT 2130
Db 1476 ----- 1475
Qy 2131 GGGCATGCCAGCGAGCAGAGCCAGACCCAGGCTGTGCGCAGAACCCGCTGCCCG 2190
Db 1476 -----CCAGCGAGCAGAGCCAGACCCAGGCTGTGCGCAGAACCCGCTGCCCG 1527
Qy 2191 TGCTCGCGGAGTCCAGGAGGGCCAGGTGCCCGGGTCAAGGGGTTCCACTCTGTGTC 2250
Db 1528 TGCTCGCGGAGTCCAGGAGGGCCAGGTGCCCGGGTCAAGGGGTTCCACTCTGTGTC 1587
Qy 2251 TACGACTGTGTGACTGCGAGCGGGCAGCTACCGGCAAAACCCAGGTTGAGCCGCTTCC 2310
Db 1588 TACGACTGTGTGACTGCGAGCGGGCAGCTACCGGCAAAAC----- 1630
Qy 2311 CGGCAGCGGGGTGGGNAACGACGAGGGAGGGTCTGCCAAGTCTGACTCTGAGACC 2370
Db 1631 ----- 1630
Qy 2371 AGAGCCACAGGTTACAAGACAAACCCAGCGGCTTCTCTCTCTCACAGACGACATC 2430
Db 1631 -----CAGACGACATC 1641
Qy 2431 GCCTGCACTTTTGTGGCAGAGTGAAGTGTCCCGGAGCGAAGCAGCTGTCTCCG 2490
Db 1642 GCCTGCACTTTTGTGGCAGAGTGAAGTGTCCCGGAGCGAAGCAGCTGTCTCCG 1701
Qy 2491 CGCAGGCTCGGTTCCGCTGGGCGAGCGGCTGTGCTGCTGCTCTCTCTGCTG 2550
Db 1702 CGCAGGCTCGGTTCCGCTGGGCGAGCGGCTGTGCTGCTGCTCTCTCTGCTG 1761
Qy 2551 AGCCTGGGCTGGGCTTGTGCTGCTGCTTGTGGGCTGTTGTTTCAACATCGGACAGC 2610
Db 1762 AGCCTGGGCTGGGCTTGTGCTGCTGCTTGTGGGCTGTTGTTTCAACATCGGACAGC 1821
Qy 2611 CCACGTGTTAGGCTCGGGGGGGCCCTCGGCTGCTTGTGGCTGCTGCTGCGGCTG 2670

Db 1822 CCACGTGTTCAGGCCTCGGGGGGGCCCTGCGCTGCTTTTGGCCCTGTGTGCTCGGGCCTG 1881
Qy 2671 GTCTGCTCAGCGCTCCTCTGTTCCCTGGCGCAGCCAGCCCTGCCCCGATGCTCGGCCAG 2730
Db 1882 GTCTGCTCAGCGCTCCTCTGTTCCCTGGCGCAGCCAGCCCTGCCCCGATGCTCGGCCAG 1941
Qy 2731 CAGCCCTTGTCCCACTCCCGCTCAGCGGCTGCTGAGCAGCACTCTTCTCTCAGCGCGGCC 2790
Db 1942 CAGCCCTTGTCCCACTCCCGCTCAGCGGCTGCTGAGCAGCACTCTTCTCTCAGCGCGGCC 2001
Qy 2791 GAGATCTGTGAGTGAAGATGCTGCTGAGCTGGGCGAGCCGCTGAGTGGTGCCTG 2850
Db 2002 GAGATCTGTGAGTGAAGATGCTGCTGAGCTGGGCGAGCCGCTGAGTGGTGCCTG 2061
Qy 2851 CGGGGGCCCTGGGCTTGGCTGCTGCTGCGCCATGCTGTGAGGTGCGACTGTGC 2910
Db 2062 CGGGGGCCCTGGGCTTGGCTGCTGCTGCGCCATGCTGTGAGGTGCGACTGTGC 2121
Qy 2911 ACCTGTACCTGTGGCTTCCCGCGGAGGTGTGACGGAATGCGCACTGCTGCCACG 2970
Db 2122 ACCTGTGTACCTGTGGCTTCCCGCGGAGGTGTGACGGAATGCGCACTGCTGCCACG 2181
Qy 2971 GAGCGCTGTGTGACTGCGGCAACGCTCCTGGGTGAGTTCGGCCTAGCGCAGCCACC 3030
Db 2182 GAGCGCTGTGTGACTGCGGCAACGCTCCTGGGTGAGTTCGGCCTAGCGCAGCCACC 2241
Qy 3031 AATGCCACGCTGGGCTTCTCTGCTTCTGCGGCACTTTCCTGTGCGGAGCAGCGGGC 3090
Db 2242 AATGCCACGCTGGGCTTCTCTGCTTCTGCGGCACTTTCCTGTGCGGAGCAGCGGGC 2301
Qy 3091 TGCTACAACTGCGGCTGCGCTCACCTTTGCCATGCTGCGCTACTTTCATCACCTGGTGC 3150
Db 2302 CGCTACAACTGCGGCTGCGCTCACCTTTGCCATGCTGCGCTACTTTCATCACCTGGTGC 2361
Qy 3151 TCCTTTGTGCGCTCCTGCGCAATGTGAGTGTCTCAGGCGCGCGTGCAGATGGGC 3210
Db 2362 TCCTTTGTGCGCTCCTGCGCAATGTGAGTGTCTCAGGCGCGCGTGCAGATGGGC 2421
Qy 3211 GCGCTCCTGCTCTGTGCTGCGGATCCTGCGCTTCCACCTGCCAGGTGTACTG 3270
Db 2422 GCGCTCCTGCTCTGTGCTGCGGATCCTGCGCTTCCACCTGCCAGGTGTACTG 2481
Qy 3271 CTATGCGGCGCAGCGGCTCAACACCCCGAGTTCCTCTGGAGGGGCGCTTGGGAT 3330
Db 2482 CTATGCGGCGCAGCGGCTCAACACCCCGAGTTCCTCTGGAGGGGCGCTTGGGAT 2541
Qy 3331 GCGCAAGGCCAGATGAGCGGAAACAGAGAAATCAGGGGAAACATGAGTGACCCAAACC-C 3389
Db 2542 GCGCAAGGCCAGATGAGCGGAAACAGAGAAATCAGGGGAAACATGAGTGACCCAAACC 2601
Qy 3390 TGTGATCTCAGCCCGGTGAACCCAGACTTAGCTGCGATCCCGCCCAAGCCAGCAATGAC 3449
Db 2602 TGTGATCTCAGCCCGGTGAACCCAGACTTAGCTGCGATCCCGCCCAAGCCAGCAATGAC 2661
Qy 3450 CCCTGTCTCGCTACAGAGACCTCCCGCTCTAGGTTCTGAGCCCGAGGTGTCTCTGACC 3509
Db 2662 CCCTGTCTCGCTACAGAGACCTCCCGCTCTAGGTTCTGAGCCCGAGGTGTCTCTGACC 2721
Qy 3510 CTGACCCC 3517
Db 2722 TGACCCCC 2729

Search completed: December 2, 2004, 10:26:09
Job time : 1120 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 2, 2004, 10:00:09 ; Search time 6934 Seconds
(without alignments)
18724.368 Million cell updates/sec

Title: US-10-035-045-20

Perfect score: 3563

Sequence: 1 agcctggcagtgccctcagg.....tggacaccctgtgaccatc 3563

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 32822875 seqs, 1821986598 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_ges1.*
9: gb_ges2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	663	18.6	684	5	BX117730	BX117730
C 2	366.4	10.3	750	5	BQ178590	BQ178590 UI-M-EVO-
C 3	288	8.1	495	4	BM706305	BM706305 UI-B-DW0-
C 4	219.2	6.2	323	2	AW417577	AW417577 54413 MAR
C 5	187.8	5.3	830	8	AZ750699	AZ750699 RPCI-24-1
C 6	154.8	4.3	168	1	AA907022	AA907022 Oj92a08.s
C 7	153	4.3	210	9	CE644804	CE644804 tigr-gss-
C 8	151.4	4.2	558	2	BE754542	BE754542 208082 MA
C 9	130.6	3.7	2373	9	AY410649	AY410649 Homo sapi
C 10	124.2	3.5	2376	9	AY410651	AY410651 Mus muscu
C 11	118.2	3.3	2373	9	AY410650	AY410650 Pan trogl
C 12	108	3.0	973	9	CNS02BUU	AL190335 Tetraodon
C 13	103.4	2.9	298	1	AI562167	AI562167 vw73d10.x
C 14	101.8	2.9	1038	9	CNS0506R	AL315180 Tetraodon
C 15	95	2.7	4444	3	AV325227	AV325227 Rattus no
C 16	93	2.6	3115	3	AK029770	AK029770 Mus muscu
C 17	90.4	2.5	2738	3	AK077434	AK077434 Mus muscu
C 18	87	2.4	938	4	BI462667	BI462667 603202107
C 19	81	2.3	525	9	CC546019	CC546019 CH240 428
C 20	77.4	2.2	612	4	BM439858	BM439858 pgrln.p0
C 21	77.2	2.2	1041	9	CNS012X1	AL174862 Tetraodon
C 22	75.6	2.1	829	9	CNS04565	AL274982 Tetraodon
C 23	74.6	2.1	641	6	CA426652	CA426652 UI-H-FP1-
C 24	74	2.1	718	8	AZ972907	AZ972907 2M0246M24

25	72.4	2.0	637	9	CE303215	tigr-gss-
C 26	71.6	2.0	699	7	CN218468	CN218468 RJA030H01
C 27	71	2.0	703	7	CO043387	CO043387 UI-M-G10-
C 28	70.8	2.0	2182	3	AK034263	Mus muscu
C 29	69.8	2.0	464	1	AA937218	AA937218 OK13f08.s
C 30	69.8	2.0	498	2	AW051287	AW051287 wv83q12.x
C 31	69.2	1.9	525	8	AZ483105	AZ483105 IM0308M03
C 32	69	1.9	644	9	CL185945	CL185945 104 400 1
C 33	69	1.9	1470	2	BE910284	BE910284 601503629
C 34	68.6	1.9	815	8	CC341366	CC341366 OGUCA43TH
C 35	68.6	1.9	820	9	CC647826	CC647826 OGUCA78TH
C 36	68.6	1.9	828	8	BZ532498	BZ532498 OGALR19TC
C 37	68.6	1.9	877	9	CG141385	CG141385 PUFO953TB
C 38	68.6	1.9	916	8	BZ532502	BZ532502 OGALR19TM
C 39	67.4	1.9	1244	4	BG846745	BG846745 1024014H0
C 40	67	1.9	562	1	AI742401	AI742401 wv40e02.x
C 41	66.6	1.9	925	9	CNS0091P	AL053013 Drosophil
C 42	66.4	1.9	925	9	CNS0091P	AL053013 Drosophil
C 43	66.2	1.9	490	6	CB725694	CB725694 AMGNNUC.N
C 44	66.2	1.9	581	6	CB606876	CB606876 AMGNNUC.N
C 45	66.2	1.9	831	7	CO394472	CO394472 AGENCOURT

ALIGNMENTS

RESULT 1	BX117730/c	BX117730	684 bp	mRNA	linear	EST 07-FEB-2003
LOCUS	BX117730	Soares NFL T GBC S1	Homo sapiens	CDNA clone		
DEFINITION	IMAGp9981153811	IMAGp9981153811	IMAGp9981153811	mRNA sequence.		
ACCESSION	BX117730					
VERSION	BX117730.1	GI:27881047				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	Ebert,D., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.					
TITLE	Human UnigeneSet - RZPD3					
JOURNAL	Unpublished (2003)					
COMMENT	Contact: Ina Rolfs					
	RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH					
	Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany					
	RZPD; IMAGp9981153811.					
	RZPDLIB; I.M.A.G.E. cDNA Clone Collection;					
	Human UnigeneSet - RZPD3 (RZPDLIB No.972)					
	http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi/response?libNo=972					
	Contact: Ina Rolfs					
	RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH					
	Heubnerweg 6, D-14059 Berlin, Germany					
	Tel: +49 30 32639 101					
	Fax: +49 30 32639 111					
	www.rzpd.de					
	This clone is available royalty-free from RZPD;					
	contact RZPD (clone@rzpd.de) for further information. Seq primer:					
	M13r, Primer sequence: TTTACACAGGAACACGTATGAC.					
FEATURES	Location/Qualifiers					
source	1..684					
	/organism="Homo sapiens"					
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	/db_xref="taxon:9606"					
	/clone="IMAGp9981153811 ; IMAGE:1505750"					
	/lab_host="DH10B"					
	/clone_lib="Soares NFL T GBC S1"					
	/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI CGAP GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as					

tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaudo. "

ORIGIN

Query Match	18.6%	Score 663;	DB 5;	Length 684;
Best Local Similarity	98.2%	Pred. No. 5.9e-119;		
Matches	663;	Conservative	0;	Mismatches 12; Indels 0; Gaps 0;
QY	1693	CCCCGCCAGACCCCGCTGAAGCCCTGCGAGGTGAGCCCGGAGATGGGGTGTGCTGTC	1752	
Db	675	CCCCGNCAGACNCCCTGAGCTGCGAGGTGAGNCCGNNATGGGGTGTGCTGTC	616	
QY	1753	CTCTGATGTGCCAGGCCACAGGCAAGCCACACGCTGAGCTGGAGTGGCTGGCG	1812	
Db	615	CTGTGATGTGCCAGGCCNCCAGGCTGCGAGGTGAGNCCGNNATGGGGTGTGCTGTC	556	
QY	1813	GCTCAGCCCGCTGCGCCCGGCGAGCTCTGGAGAACATGTACAACTGACCTTCCACGT	1872	
Db	555	GCTCAGCCCGCTGCGCCCGGCGAGCTCTGGAGAACATGTACAACTGACCTTCCACGT	496	
QY	1873	GGCGGGCTGCGCTGCGTTCGACAGCAGCGGAAAGCTGACATGAGTACGACCTGAA	1932	
Db	495	GGCGGGCTGCGCTGCGTTCGACAGCAGCGGAAAGCTGACATGAGTACGACCTGAA	436	
QY	1933	GCTGTGGTGTGGCAGGCTCAGTGCAGGCTCAGCAAGCTGCGGCTTCAACGGCAG	1992	
Db	435	GCTGTGGTGTGGCAGGCTCAGTGCAGGCTCAGCAAGCTGCGGCTTCAACGGCAG	376	
QY	1993	CCTCAGACAGAGCCCTGAGATCCGCTGACACAGCTCTGACACAGAGTGGTGAAG	2052	
Db	375	CCTCAGACAGAGCCCTGAGATCCGCTGACACAGCTCTGACACAGAGTGGTGAAG	316	
QY	2053	GTGGTGTGCCAGGCTGCTCCGCTGTAGTCCCGCGGCGAGGCGGAGCTGGGGTGGG	2112	
Db	315	GTGGTGTGCCAGGCTGCTCCGCTGTAGTCCCGCGGCGAGGCGGAGCTGGGGTGGG	256	
QY	2113	GCGTTCAGTCTCCGCTGGGATGCCAGCCGAGCAGAGCCAGCCCGGCTGTGCG	2172	
Db	255	GCGTTCAGTCTCCGCTGGGATGCCAGCCGAGCAGAGCCAGCCCGGCTGTGCG	196	
QY	2173	CAGAGCCCGTGTCCCGTGTGCGGAGTCCAGAGGAGGCGAGTCCCGGCTCAAG	2232	
Db	195	CAGAGCCCGTGTCCCGTGTGCGGAGTCCAGAGGAGGCGAGTCCCGGCTCAAG	136	
QY	2233	GGTTTCCACTCTGCTGTGCTAGTGTGTGAGTCTGCGAGGCGGCGAGTACCGGCAAAAC	2292	
Db	135	GGTTTCCACTCTGCTGTGCTAGTGTGTGAGTCTGCGAGGCGGCGAGTACCGGCAAAAC	76	
QY	2293	CCAGTGTGAGCCCTTCCCGAGCGGGGTGGGAAAGCAGCAGGAGGCTCTGCGCA	2352	
Db	75	CCAGTGTGAGCCCTTCCCGAGCGGGGTGGGAAAGCAGCAGGAGGCTCTGCGCA	16	
QY	2353	AGTCTGACTCTGAG	2367	
Db	15	AGTCTGACTCTGAG	1	

RESULT 2
 LOCUS BQ178590/c
 DEFINITION UI-M-EVO-bws-h-23-0-UI.r1 NIH_BMAP_EVO Mus musculus cDNA clone
 IMAGE:5701318 5', mRNA sequence.
 ACCESSION BQ178590
 VERSION BQ178590.1 GI:20354082
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

1 (bases 1 to 750)
 NIH-MGC <http://imgc.ncbi.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-f@mail.nih.gov
 Tissue Procurement: Dr. James Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

Seq primer: pYX-5.

FEATURES
 source

Location/Qualifiers
 1..750
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGR:5701318"
 /tissue_type="whole brain"
 /dev_stage="embryo 15.5 dpc"
 /lab_host="DH10B (TI phage resistant)"
 /clone_lib="NIH_BMAP_EVO"
 /note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according to
 Bonaudo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured mRNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with an
 oligo-dT primer containing a Not I site. Double stranded
 cDNA was size selected according to mRNA size fraction,
 ligated with EcoR I adaptor, digested with Not I, and then
 cloned directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA
 tail, is GTGGCTGGAA. This library was created for the
 University of Iowa Mouse Brain Molecular Anatomy Project
 (BMAP). 'Gene Discovery in the Developing Mouse Nervous
 System', supported by National Institutes of Mental Health
 (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match	10.3%	Score 366.4;	DB 5;	Length 750;
Best Local Similarity	72.9%	Pred. No. 5e-61;		
Matches	485;	Conservative	0;	Mismatches 177; Indels 3; Gaps 1;
QY	938	CAGGTACGTACGGTGTAGCATGAGCTGTGAGCGCCCGGAGACCTTCCCTTCCTTC	997	
Db	654	CAGGTACGTATAGTGGCAGCATGGATCGGNTAAGTGACCGGGAAACGTTTCCATCCTTC	605	
QY	998	TTCCGACCGTGTCCAGCGACCGCTGTGAGCTGAGCGCGCGGAGCTGTGCAGGAG	1057	
Db	604	TTCCGACAGTGTCCAGTGTGAGCGCGCTGTGAGCTGTGAGCTGTGAGCTGTGAG	545	
QY	1058	TTCCGCTGGAATGGTGGCGCCCTGGCGACGACGACGAGTACGGCGGCGAGGCTGTG	1117	
Db	544	TTCCGCTGGAATGGTGGCGCCCTTAGGGAGTGTGATGATGATGATGATGATGATGATG	485	
QY	1118	AGCATCTTCTGGCCCTGCGCGCAGCGCATCTGCATCGCGCAGGAGGCTGTG	1177	
Db	484	AGCATCTTCTTCTAGTCTGGCCAAATGACAGAGTATCTGCATCGCATGAGGCTGTG	425	
QY	1178	CGCTGCGCCGTCGCGATGACTCGCGGCTGGGGAAGTGTGAGGAGCTGTGACAGG	1237	
Db	424	CCACAAATGACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG	365	
QY	1238	AACAGAGCAGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG	1297	
Db	364	AACCAAGTAAAGTAAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG	305	
QY	1298	TTCAACTACGATCAGCAGCAGGCTCTCGCCCAAGGTGTGGTGTGGCCAGGAGGCTGTG	1357	

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Db      304  TTTAGTTACAGCATCCATCATGCGCTCTCACCAGGTATGGTGGCCAGTCTTGG 245
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QY      1418 TTCTCTCAGAGGGTGCACAGCTGACAGTTCCTCCAGTACGTGAAGACGACCTGGCC 1477
Db      184  TTTTTCAGCGGGTGCCTTACTGCTGCTGAATTTTCCCATTTATGTGGAGACTCACCTTGC 125
QY      1478 CTGGCCACCGACCGCGCTCTGCTCTGCTGCGCTGGCGAGGAGGAGCGTCTGGAGGAG 1537
Db      124  CTGGCCGCTGACCCAGCAATCTCTGCTCTCACTG---AATGCGAGTTGGATCTGGAGAA 68
QY      1538 GACGTGTGGCGGCGAGCGCTGCCCGCAGTGTGACTGCATCAGCTGCAGAACGTCGAGCGCA 1597
Db      67  CATGTGATGGGCAAGCGCTGTCACCGTGTGACGACATCATGTCTGAGAACCTATCATCT 8
QY      1598 GGGCT 1602
Db      7  GGGCT 3

RESULT 3
BM706305
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

BM706305
495 bp mRNA linear EST 28-FEB-2002
UI-E-DW0-agh-a-22-0-UI-r1 UI-E-DW0 Homo sapiens cDNA clone
UI-E-DW0-agh-a-22-0-UI 5', mRNA sequence.
BM706305
BM706305.1 GI:19019563
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 495)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
9704477
8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="UI-E-DW0-agh-a-22-0-UI"
/tissue_type="lens"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-DW0"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-DW0 is a cDNA library containing the following
tissue(s): lens. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an

```

oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGATTAGCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

ORIGIN

```

Query Match      8.1%; Score 288; DB 4; Length 495;
Best Local Similarity 100.0%; Pred. No. 9.9e-46;
Matches 288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3276 GGGGAGCGAGGGCTCAACACCCCGAGTTCCTTGGAGGGGGCCCTGGGGATGCCCCA 3335
Db      1  GGGGAGCGAGGGCTCAACACCCCGAGTTCCTTGGAGGGGGCCCTGGGGATGCCCCA 60

QY      3336 AGCCAGATGACGGGACACAGAGAAATCAGGGGAAACATGATGACCCCAACCTGTGAT 3395
Db      61  AGCCAGATGACGGGACACAGAGAAATCAGGGGAAACATGATGACCCCAACCTGTGAT 120

QY      3396 CTCAGCCCGGTGAACCCAGACTTAGTCTCGATCCCCCCCCAGCCAGCAATGACCGTCT 3455
Db      121  CTCAGCCCGGTGAACCCAGACTTAGTCTCGATCCCCCCCCAGCCAGCAATGACCGTCT 180

QY      3456 CTCGCTACAGAGACCCCTCCCGTCTAGGTTCCTGACCCCAAGTTGTCTCTGACCCCTGACC 3515
Db      181  CTCGCTACAGAGACCCCTCCCGTCTAGGTTCCTGACCCCAAGTTGTCTCTGACCCCTGACC 240

QY      3516 CCACAGTGGCCCTAGGCTGAGGACGTCGAGCACGTCGACACCCCTGTGACCATC 3563
Db      241  CCACAGTGGCCCTAGGCTGAGGACGTCGAGCACGTCGACACCCCTGTGACCATC 288

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RESULT 4

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AW417577
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

AW417577
54413 MARC lPIG Sus scrofa cDNA 5', mRNA sequence.
AW417577.1 GI:6945459
EST.
Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 323)
Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
Vallet,J., Wise,T., Rohrer,G.A., Pettea,G., Sultana,R.,
Quackenbush,J. and Keeler,J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)
22213789
12226715
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGTCACGACG
Plate: 20 row: E column: 14
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1. .323
/organism="Sus scrofa"

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/tissue_type="pooled"
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/notes="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."

ORIGIN

Query Match 6.2%; Score 219.2; DB 2; Length 323;
Best Local Similarity 82.3%; Pred. No. 2.6e-32;
Matches 251; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
QY 2949 GGAAGTGGACATGCTGCTCCAGGAGGCGCTGTGCACTGGCGCACACGCTCTCTGGGTCAG 3008
|||||
DB 19 GGAAGTGGCGTGGCTACCCACANAGGCACTGGTGCATGGCGGCTGCACCTCTGGATCAG 78
QY 3009 CTTGCGGCTAGCGCAGCCACCAATGCAAGCTGGCCTTTCTCTGCTTCTCTGGGCACTTT 3068
|||||
DB 79 CTTGAGCTGGTACATGCTGCCAATGCCAGCTGGCTTTCTCTGCTTCTCTGGGCACTTT 138
QY 3069 CTTGCTGGAGGAGCAGCGGCTGCTACACCGTGGCGGCTGCTGCTGCTGCTGCTGCTGCT 3128
|||||
DB 139 CTTGCTGGAGGAGCAGCGGCTGCTACACCGTGGCGGCTGCTGCTGCTGCTGCTGCTGCT 198
QY 3129 GGCCTACTTATCATCTGGTGGTCTCTTTGTCCTCTCTGCTGCTGCTGCTGCTGCTGCT 3188
|||||
DB 199 GGCCTACTTATCATCTGGTGGTCTCTTTGTCCTCTCTGCTGCTGCTGCTGCTGCTGCT 258
QY 3189 CAGGCGCGGCTGTCAGATGGCGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3248
|||||
DB 259 CCAGCTGCTGTCATGCTGGTGGCGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 318
QY 3249 CCACC 3253
DB 319 CCACC 323

RESULT 5

AZ750699
LOCUS
DEFINITION
830 bp DNA linear GSS 25-JAN-2001
RPCI-24-112J8-TV RPCI-24 Mus musculus genomic clone RPCI-24-112J8,
genomic survey sequence.

ACCESSION
AZ750699
VERSION
AZ750699.1 GI:12535858
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Bases 1 to 830)
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M.,
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregorgis, E.,
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)

TITLE

JOURNAL
COMMENT
Other_GSSs: RPCI-24-112J8.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@igir.org

Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 112 row: J column: 8
Seq primer: T7
Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..830
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-112J8"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI;
RPCI-24 Mouse BAC library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamHI sites using MboI partially digested male C57BL/6J
DNA."

ORIGIN

Query Match 5.3%; Score 187.8; DB 8; Length 830;
Best Local Similarity 58.5%; Pred. No. 3.8e-26;
Matches 430; Conservative 0; Mismatches 257; Indels 48; Gaps 4;
QY 1579 GCTGCAGAACGTCGAGCGCAGGGCTAAATCACACACGACGCTTCTCTCTACGACGCTGT 1638
DB 43 GTTGCAGAACTATCAGCTGGCAATTGACACCACTAAATTTGCAACCTTATGACGCTGT 102
QY 1639 GTATAGCTGGCCAGGCTGTCACACACTCTTTCAGTGCACGCTTACGCTGCGCCGCGC 1698
DB 103 GTACAGTGTGGCTCAAGCCCTTCACACACCTTACAGTGCATATGTCACATTCGCCAGT 162
QY 1699 GCAGGACCCGCTGAAGCCCTGGCAGGTGAGCCGGGAGATGGGGTGTGCTGTCTCTCTGC 1758
DB 163 ATCAGAAATATGTTTACCTCTGGCAGGTAGGGTGGTGGTGGTGGTGGTGGTGGTGGT 218
QY 1759 ATGTGCCCGACGCCACAGGCAAGCCACAGCCCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1816
DB 219 TGCTCTGCAGGAACACTGAACACAGGCGCAGAGCCAAATCTTGTGTGCTGAGTGGAGG 278
QY 1817 AGCCCGCTGCCCGCGCAGCTCTCTGGAGAACATGTACACCTGACCTTCCACGCTGGCG 1876
DB 279 TACCTGACTCTCACTCCACAGCTCTCTGGAGAACATGTACAAATATGAGTTTCCATGCTCG 338
QY 1877 GGGCTGCGCTGCGCTTCGACAGCAGCGGAACTGGACATGGAGTACAGCTGAAGCTG 1936
DB 339 GACTTGACACTACAGTTTGTGCTGAAGGGAATGTAGACATGGAATATGACCTGAAGATG 398
QY 1937 TGGGTGTGGCAGGGCTCAGTCCCGCAGGCTCCACAGCTGGCGCAGGTTTCAACGCGACCTC 1996
DB 399 TGGGTGTGGCAGAGCCCTACACCTGTATTACATATCTGTGGGCACCTTCAACGCGACCTC 458
QY 1997 AGGACAGAGCGCTGAAGATCCGCTGGCAGCAGCTGTGACACACAGGCTGAGGTGAGGTTG 2056
DB 459 CAGCTGCAGCAGTCTAAATATGTCTGGC-----CAGGCAACACAGGTAAAGGACAAAGACAG 512
QY 2057 GTGTGCCAGGGCTGCCCGTGTAGCCCGCGGCGAGGCGCAGGCTGGGGGTGGGGGCGCG 2116
DB 513 GCAAAAGAGTGTGGGTAGAGCTTGTGGTCTTGGGCCAGTGTAGCCAGGGG---- 568
QY 2117 TTCCAGTCTCCCGTGGGCATGCCAGCGAGCAGAGCCAGACCCCGAGGCTGTGGCGCAGA 2176
DB 569 -----AGGCTTAACCCCAAGGCTCCATGTACAGG 596
QY 2177 AGCCCGTGTCCCGTGTCTCGCGGCACTGCCAGGAGGCGCAGGTGCGCGGGTCAAGGGGT 2236
DB 597 TGCCAGTCTCCCGAGTGTCCCGCCAGTGCAGAGATGGCCAGGTTCCCGGAGTAAAGGGCT 656
QY 2237 TCACCTCTCTGCTTACGACTGTGTGGACTGTGGAGCTGGAGCGGCGGCGAGCTACCGGCAAAACCCAG 2296
DB 657 TTCATTCTCTGCTCTATGACTGCGTGGAGTGCAGAGCGGCGCAGCTACCGGAGCATTCAG 716
QY 2297 GTGAGCGCGCTTCCC 2311
DB 717 GTGAACCGCTTTTCC 731

```

RESULT 6
AA907022      168 bp      mRNA      linear      EST 19-MAY-1998
LOCUS         o192a08_s2 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
DEFINITION    IMAGE:1505750 3', mRNA sequence.
ACCESSION     AA907022      1 GI:3042482
VERSION       AA907022.1
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 168)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 825 Std Error: 0.00
Seq primer: -40ml3 fwd. EF from Amersham
High quality sequence stop: 157.
Location/Qualifiers
1..168
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1505750"
/lab_host="DH10B"
/clone_lib="Soares NFL T_GBC_S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHR, and B-cell
NCI CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
1.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
```

Query Match 4.3%; Score 154.8; DB 1; Length 168;
Best Local Similarity 98.7%; Pred. No. 9.3e-20;
Matches 156; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1619 TTCTGTCTACGAGCTGTGTATAGCGTGGCCGAGCCCTGCACAACTCTTCAGTGC 1678
Db 11 TTTTGTCTACGAGCTGTGTATAGCTGGCCGAGCCCTGCACAACTCTTCAGTGC 70

QY 1679 AACGCTCAGGTGCCCCGCGCAGACCCGCGTGAAGCCCTGGCAGGTGAGCCCGGAGAT 1738
Db 71 AACGCTCAGGTGCCCCGCGCAGACCCGCGTGAAGCCCTGGCAGGTGAGCCCGGAGAT 130

QY 1739 GGGGGTGTGCTCTCTGTCATGTCGCCAGGCCAGCCAG 1776
Db 131 GGGGGTGTGCTCTCTGTCATGTCGCCAGGCCAGCCAG 168

RESULT 7
CE644804
LOCUS tigr-gss-dog-17000367133648 Dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.
ACCESSION CE644804
VERSION CE644804.1 GI:36963644
KEYWORDS GSS.
SOURCE Canis familiaris (dog)

Query Match 4.3%; Score 154.8; DB 1; Length 168;
Best Local Similarity 98.7%; Pred. No. 9.3e-20;
Matches 156; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1619 TTCTGTCTACGAGCTGTGTATAGCGTGGCCGAGCCCTGCACAACTCTTCAGTGC 1678
Db 11 TTTTGTCTACGAGCTGTGTATAGCTGGCCGAGCCCTGCACAACTCTTCAGTGC 70

QY 1679 AACGCTCAGGTGCCCCGCGCAGACCCGCGTGAAGCCCTGGCAGGTGAGCCCGGAGAT 1738
Db 71 AACGCTCAGGTGCCCCGCGCAGACCCGCGTGAAGCCCTGGCAGGTGAGCCCGGAGAT 130

QY 1739 GGGGGTGTGCTCTCTGTCATGTCGCCAGGCCAGCCAG 1776
Db 131 GGGGGTGTGCTCTCTGTCATGTCGCCAGGCCAGCCAG 168

RESULT 8
BE754542
LOCUS 208082 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION ACCESSION BE754542
VERSION BE754542.1 GI:10168534
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 558)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrnkug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keefe, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)

Query Match 4.3%; Score 153; DB 9; Length 210;
Best Local Similarity 83.3%; Pred. No. 2.1e-19;
Matches 174; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 3010 TTCGCCCTAGTGCGACCGCCACCAATGCCAGTGGCTTTCTGCTTCTGGGCACTTTC 3069
Db 1 TTTGGCCTAGTGCGATGCCATCAATGCCATGCTGGCTTCTGCTTCTGGGCACTTTC 60

QY 3070 CTGGTGGCGAGCCAGCCGGCTGTCTACACCGTGGCGGCTCACCTTTCGCGATGCG 3129
Db 61 TTGGGGCAGAGCCGCGCGGCTGTCTCTTTGTCCTCTCTTTGTCCTCTCTTTGTCCTCT 120

QY 3130 GCCTACTTTCATCACCCTGGTGTCTCTTTGTCCTCTCTTTGTCCTCTCTTTGTCCTCT 3189
Db 121 GCCTACTTTCATCACCCTGGTGTCTCTTTGTCCTCTCTTTGTCCTCTCTTTGTCCTCT 180

QY 3190 AGGCCCGCGCTGCAGATGGCGCCCTCT 3218
Db 181 CAGCCCACTGTGCAGATGGCGCCATCTCT 209

Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 210)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
22875432
14512627
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1..210
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site_1: BstXI; Libraries were prepared from
peripheral blood"

Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 210)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
22875432
14512627
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1..210
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
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/clone_lib="Dog Library"
/note="Site_1: BstXI; Libraries were prepared from
peripheral blood"

Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 210)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
22875432
14512627
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1..210
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site_1: BstXI; Libraries were prepared from
peripheral blood"

11282978	CONTACT: SMITH TPL	JOURNAL
	USDA, ARS, US Meat Animal Research Center	PUBMED
	PO Box 166, Clay Center, NE 68933-0166, USA	REFERENCE
		AUTHORS
COMMENT		

FEATURES source

ORIGIN

	Query Match	4.23;	Score 151.4;	DB 2;	Length 558;
	Best Local Similarity	76.8;	Pred. No. 4.9e-19;		
	Matches 185;	Conservative 0;	Mismatches 56;	Indels 0;	Gaps 0;
Qy	2416	CTCACACGACATCGCGTGCACCTTTTGTGGCCAGGATGAGTGGTCCCCGGGAGCGAAGC	2475		
Db	318	CACCCAGACATGSCCTCTCGCAGCAATGTGTGACGAGACCAGTGGTCCCCCAGACGGTAGT	377		
Qy	2476	ACACGCTGCTTCGCGCCGACAGTCTCGGTTCTTGGCATGGGGCGAGCCGGCTGTGCTGCTG	2535		
Db	378	ACCGGTGCTTCCCCCGCAGGCCACAGGTTCTCGCGTGGGGGAGCCGGCTGTGCTTGGG	437		
Qy	2536	CTGCTCTGCTGCTGAGCCTGGCGCTGCTGCTGCTGCTGCTTTTGGGGCTGTTCGTT	2595		
Db	438	CTGCTCTGCTGCTGGGCGATCGTTCTGAGTCTGTGCTGTGGGCGCTTTCACC	497		
Qy	2596	CACCATCGGACAGCCCACTGGTTTCAGCGCTTCGGGGGGGGCCCTTGGGCTGCTTGGCGCTG	2655		
Db	498	TGGACATCGGACAGCCCACTAGTTTCAGGCGCAGCGGAGACCCCGGGCGCTGCTCGGCGCTG	557		

RESULT 9	
AY410649	
LOCUS	
DEFINITION	AY410649 Homo sapiens TAS1R1 gene, VIRTUAL TRANSCRIPT, partial sequence, 2373 bp DNA linear GSS 16-DEC-2003
ACCESSION	AY410649
VERSION	AY410649.1 GI:39766617
KEYWORDS	GSS.

REFERENCE
AUTHORS

TITLE

JOURNAL	Science 302 (5652), 1960-1963 (2003)
PURNED	14671302
REFERENCE	2 (bases 1 to 2373)
AUTHORS	Clark, A.G., Tanenbaum, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferritera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.C., Adams, M.D. and Cargill, M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment
FEATURES	Location/Qualifiers
source	1..2373
	/organism="Homo sapiens"
	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
gene	<1..-2373
	/gene="TAS1R1"
	/locus_tag="HCM3961"

Query Match	3.7%;	Score 130.6;	DB 9;	Length 2373;
Best Local Similarity	53.7%;	Pred. No. 6.2e-15;		
Matches	296;	Conservative	0;	Mismatches 249; Indels 6; Gaps 17;
Qy	869	GAGAATGCTACATGCACCCACCCAGCCCTGCCCTGGGAGCCCTGTGTGTCAGAAAGATGCTC	928	
Db	427	GTGATTGGGCTTGACAGACCAACCGTGTGTGCCACACAGCCGCCCTGTGTGAGCCCTTTC	486	
Qy	929	TTGGCCCTTGACAGCTCAGCTACGGTGTGTAGCATGGAGCTGTGACGCGCCCGGAGACCTTC	988	
Db	487	CTGGTCCCATGATTAGCTATGCGGCCAGCAGCAGACGCTCAGCGTGAAGCGGCAGTAT	546	
Qy	989	CCCTCCCTTTCGCGACCGTGCACCGACCGACCGTGTGTCAGCTGACGCGCCGCCGCGAGCTG	1048	
Db	547	CCCTCTTTCTCGCGCACCATCCCAATGACAAGTACCAGGTGGAGACCATGTGTGCTGCTG	606	
Qy	1049	CTGCAGAGATTGCGCTGGAACTGGTGGCGCCCTGGGCACGCACGACGAGTACGGCCGG	1108	
Db	607	CTGCAGAAATTCGGGTGGACCTGGATCTCTCTGTGTGGCAGCAGTACGACACTATGGGCAG	666	
Qy	1109	CAGGGCTGAGCATCTTCTCGCGCCCTGGCGCGCGCACGCGCGCATCTGCATCGCGCACGAG	1168	
Db	667	CTAGGGGTGAGGCACTGGAGAACGACGCCCATGTGTCAGGGGATCTGCATTGCTTCAAG	726	
Qy	1169	GGCCTGTGTGCGCTGCCCCGTGCCGATGACTCGCGCTGGGGAAAGTGCAGGACGTCTCT	1228	
Db	727	GACAT-----CATGCTCTTCTCTGCCAGCTGGGGGATGAGAGGATGCAGTGCTCATG	780	

RESULT 10	
AY410651	
LOCUS	
DEFINITION	
ACCESSION	

Qy	2515	GCGAGCGGCTGTGCTGCCTGGTCCCTGCTGCTGAGCCTGGCGCTGGGCCCTTGTCGTG	2574
Dδ	340	AAGACACCTTTGCYGGGTTCTCATGGCCTTCTCACCTCGGCATCCTCCTGTGCCTG	399
Qy	2575	GCTGCTTTGGGGCTGTGTTCACTACCATCGGGACAGCCCCACTGTTTCAGGCTCTGGGGGGG	2634
Dδ	400	TWGCATCGGCTCTGTTTCTGTATACGGGGACATCCGGTGTGTGAAGGACAGAGGGGGA	459
Qy	2635	CCCTGGCTGCTTTGGCTCTGGTGTGCTGGGCTGTGCTGCTCAGCGTCTCCTCTGTC	2694

Qy	2695	CCTGGCCAGCCAGCCCTGCGCCGATGCTGGCCGAGCAGCCCTGTGCCACCTCCCGCTC	2754
Db	520	GTGGCCGAGCAGCAGAACTCCAGTGCAAGCCCGCCAGGTGCTCTCGGCATCAGCTTC	579
Qy	2755	ACGGGCTGCCTGAGCACACTCTTCTCCTCAGCGCCGAGATCTTCGTGGAGTCAGAACTG	2814

580	ACTCTGTGTATCTCTGATCTCTGGTCAAGACTTTCAGATCTCTGCTAGCTCCAGTTC	639
DB		
2815	CCTCTGAGCTGGGCAGACCGCTCAGTGGTCTGCTGCGGGGGCCCTGGGCGCTGGCTGGTG	2874
QY		
640	AACCCGGGCTGCAGGACGTGCTGAGGAAGATCTATC---GGCCGTACGGCCATCATCACC	696
DB		
2875	GTGCTGTGGCCATGCTGTGGAGGTGCACTGTGCACCTGGTACCTGGTGGCCTTCCTCCG	2934
QY		

DB	697	GTCTGCGTGGCTTTCGACAGCGGTGATC-----TGCATCTGCTGGCTGGTGCCTCTCAAGAC	730
QY	2935	CCGAGAGTGGTGA CGGACTGCATGTCGCCACGAGGCGCTGGTGCACTGCCGCACA	2994
DB	751	CCGTCAATACACCATCGGCGAAG-----CGACCACCTCTTTGATGCACTGCCACGAA	804
QY	2995	CGTCTCTGGGTGACGTTTCGGCGCTAGCGACGCCACCAATGCCACGCTGG--CGTTTCTCTG	3053

DB	805	AAC	TG	TAC	TGG	GCT	TTC	GCG	GAT	GTG	TGG	GCT	TAC	TG	CGC	CTC	TG	CGC	CTT	TG	TG	G	864
QY	3054	CTT	CT	TGG	CA	CTT	TCT	TGT	GTG	CG	GAG	CAG	CGG	GCT	TAC	AA	CCG	TG	CCG	CG	CG	GCT	3112
DB	865	CTT	CT	TGT	TCT	TCA	AGG	SG	CGA	AA	TW	ACG	GAG	CAG	TAC	AA	CG	AGG	CA	AGT	TTC	924	
QY	3114	CAC	CTT	TG	CCAT	GTG	CG	CTA	CTT	CA	CC	TGG	CT	TCC	TTT	TG	GC						

Db	925	CACCTTCAGCATGCTGTGTACCTCAATTCCTGGCTGCTCTTTSTTC	972
RESULT 13	AI562167/c		
LOCUS	AI562167	298 bp	linear
DEFINITION	vw73d10.x1 Stratagene mouse heart (#937316) Mus musculus cDNA Clone IMAGE:1260595 3', similar to SW:CA5R HUMAN P41180 EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR ; mRNA sequence.		
ACCESSION	AI562167	1	GI:451312
VERSION	AI562167.1		
KEYWORDS	EST.		

SOURCE	ORGANISM	REFERENCE	AUTHORS
Mus musculus (house mouse)	Mus musculus	1 (bases 1 to 298)	Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wyllie, T., Underwood, K., Stepto, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swallow, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			

TITLE
JOURNAL
COMMENT

Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:663147

This clone was previously sequenced on the 5' end only, this new data is from the 3' end
possible reversed clone: similarity on wrong strand
Possible reversed clone: polyt not found
High quality sequence stop: 286.

FEATURES

Location/Qualifiers
1..298
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NIH Swiss"
/db_xref="taxon:10090"
/clone="IMAGE:1360595"
/sex="pooled"
/tissue_type="heart"
/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse heart (#937316)"
/note="Organ: heart; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. 93 pooled NIH/Swiss 13 day embryo hearts. Average insert size: 1.0 Kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTT 3'."

ORIGIN

Query Match 2.9%; Score 103.4; DB 1; Length 298;
Best Local Similarity 63.5%; Pred. No. 1.1e-09;
Matches 158; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
QY 938 CAGGTGAGTACGCTGCTGATGGAGCTGCTGAGCGCCGGGAGACCTTCCCTCTCTTC 997
DB |||||
DB 295 CAGGTGAGTACGCTGATGGAGCGACGCTGATCTCAGTGGGAGCGAGTTCCGCTCTTC 236
QY 998 TTCGACACCGTCCGACGACCGTGTGACGCTGACGCGCCCGGAGCTGTGCGAGGAG 1057
DB |||||
DB 235 TTGCGCACCATCCCGACGATAGTACGAGTGGAGTATAGTGGCGTGTGCGAGAGC 176
QY 1058 TTGCGCTGGAACCTGGTGGCGCCCTGGGACGAGCAGACGATACGGCGCGGAGGCTG 1117
DB |||||
DB 175 TTGCGCTGGTCTGGATCTGCTGCTGTTGGCAGCTATGCTGACTACGCGGAGCTGGGCGTA 116
QY 1118 AGCATCTTCTGCGCCCTGGCGCGGACGCGGATCTGATCGCATCGCAGGAGGCGCTGG 1177
DB |||||
DB 115 CAGGCGCTGGAGAGCTGGCCATCCACGGGGATCTGCTGCTCCCTTCAAGGACGTGGTG 117
QY 1178 CGCTGCC 1186
DB |||||
DB 55 CCTCTCTCC 47

RESULT 14

CNS0506R/c

LOCUS

DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 006M17 of library B from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AL315180.1 GI:9548068
GSS: genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE

AUTHORS

Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis

TITLE

using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
20296633
10835645

REFERENCE

AUTHORS

Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

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TITLE

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 2, 2004, 13:08:50 ; Search time 1164 Seconds
(without alignments)
16819.604 Million cell updates/sec

Title: US-10-035-045-20

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Gapop 10.0 , Gapext 1.0

Searched: 3694831 seqs, 2747406616 residues

Total number of hits satisfying chosen parameters: 7389662

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Maximum DB seq length: 2000000000

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	3563	100.0	3563	18	US-10-725-276-20
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ALIGNMENTS

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; Sequence 20, Application US/09799629
; Publication No. US20030008344A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: LI, XIADONG, SHAWN
; APPLICANT: O'CONNELL, SHAWN
; TITLE OF INVENTION: TIR TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0277870/RXT
; CURRENT APPLICATION NUMBER: US/09/799,629
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: 60/187,546
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/195,536
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/209,840
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 60/214,213
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/226,448
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/259,227
; PRIOR FILING DATE: 2001-01-03
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
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; TYPE: DNA
; ORGANISM: Homo sapiens
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RESULT 2

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 ; Sequence 20, Application US/10035045
 ; Publication No. US20030054448A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ADLER, JON ELLIOT
 ; APPLICANT: LI, XIAODONG
 ; APPLICANT: STASZEWSKI, LENA
 ; APPLICANT: O'CONNELL, SHAWN
 ; APPLICANT: ZOZULYA, SERGEY
 ; TITLE OF INVENTION: TIR TASTE RECEPTORS AND GENES ENCODING SAME
 ; FILE REFERENCE: 078003-0280681
 ; CURRENT APPLICATION NUMBER: US/10/035,045
 ; CURRENT FILING DATE: 2002-01-03
 ; PRIOR APPLICATION NUMBER: 60/259,227
 ; PRIOR FILING DATE: 2001-01-03
 ; PRIOR APPLICATION NUMBER: 60/284,547
 ; PRIOR FILING DATE: 2001-04-19
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 3563
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-035-045-20

Query Match 100.0%; Score 3563; DB 14; Length 3563;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGCAGTGGCTCAGGCGAGTCTGACGCGCACAACTTTTCAGGCCCGAGGAGCGA 60
 Db 1 AGCTGGCAGTGGCTCAGGCGAGTCTGACGCGCACAACTTTTCAGGCCCGAGGAGCGA 60
 QY 61 GGACACCACTGGGGGCCCGAGGGTGTGGCAAGTGGAGTGGCAAGGTTTGTCTAAACAAA 120
 Db 61 GGACACCACTGGGGGCCCGAGGGTGTGGCAAGTGGAGTGGCAAGGTTTGTCTAAACAAA 120
 QY 121 TCCTCTGCGCTCCCGCCCGCGCTCACTCCATGTAGGCCCGCAGTCGGGGCAGCCAC 180
 Db 121 TCCTCTGCGCTCCCGCCCGCGCTCACTCCATGTAGGCCCGCAGTCGGGGCAGCCAC 180
 QY 181 CTGCGGTGCTGTTGGAAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 Db 181 CTGCGGTGCTGTTGGAAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 241 CTCTGGGCTCTCTCTGCACTTGGGACGGGGCGCCCATTTGTCCTGTGTACAGCAACTTAGG 300
 Db 241 CTCTGGGCTCTCTCTGCACTTGGGACGGGGCGCCCATTTGTCCTGTGTACAGCAACTTAGG 300

Db	241	CTCTGGGCTCTCTCTGACACCTGGGACGGGGGCCCCATTGTGCTCTGTACACAGCAACTTAGG	300
Qy	301	ATGAGGGGAGCTACCTGCTGGGGGGCTCTTCCCTCTGGGCGAGGCCGAGGAGGCTGGC	360
Db	301	ATGAGGGGAGCTACCTGCTGGGGGGGCTGTTCCTCTGGGCGAGGCCGAGGAGGCTGGC	360
Qy	361	CTCCGACGCGGACACGGGCCAGCAGCCCTGTGTGACACCAAGGTACAGAGGTGGGACGGCC	420
Db	361	CTCCGACGCGGACACGGGCCAGCAGCCCTGTGTGACACCAAGGTACAGAGGTGGGACGGCC	420
Qy	421	TGGGTGGGGTTCAGGGGTGAACAGGTCTGGGGTGTCTCTGAGCTGGGGCCGAGGTTGGCCAT	480
Db	421	TGGGTGGGGTTCAGGGGTGAACAGGTCTGGGGTGTCTCTGAGCTGGGGCCGAGGTTGGCCAT	480
Qy	481	CTGGGTTCTGTGTGGGCCCGCAGGTTCTCTCAACAGCCCTGCTCTGGGCACTGGCCATGA	540
Db	481	CTGGGTTCTGTGTGGGCCCGCAGGTTCTCTCAACAGCCCTGCTCTGGGCACTGGCCATGA	540
Qy	541	AAATGGCCGTGGAGGAGATCAACAAAGTGGATCTGCTGCCCGGCTGCGCTGGGCT	600
Db	541	AAATGGCCGTGGAGGAGATCAACAAAGTGGATCTGCTGCCCGGCTGCGCTGGGCT	600
Qy	601	ACGACTCTTTGATACGTGTCGAGCTGAGGCTGTGTGGGCGATGAAGCCAGGCTCATGTTC	660
Db	601	ACGACTCTTTGATACGTGTCGAGCTGAGGCTGTGTGGGCGATGAAGCCAGGCTCATGTTC	660
Qy	661	TGGCCAGGAGGAGGAGGAGGAGATCGCGCTACTCAACTACAGCAGTACACAGCCC	720
Db	661	TGGCCAGGAGGAGGAGGAGGAGATCGCGCTACTCAACTACAGCAGTACACAGCCC	720
Qy	721	GTGTGCTGGCTCATCGGGGCCCACTCGTTCAGAGCTCGCCATGGTCAACGGCAAGTTCT	780
Db	721	GTGTGCTGGCTCATCGGGGCCCACTCGTTCAGAGCTCGCCATGGTCAACGGCAAGTTCT	780
Qy	781	TCAGCTTCTTCTCATGCCCCAGTGGGGGCCCCCACCATACAGCAGTACACCAACC	840
Db	781	TCAGCTTCTTCTCATGCCCCAGTGGGGGCCCCCACCATACAGCAGTACACCAACC	840
Qy	841	CCTGCCCGTGGGAGCCCTTGTGTACAGAGAAATGTACATGACACCCACCCAGCCCTGC	900
Db	841	CCTGCCCGTGGGAGCCCTTGTGTACAGAGAAATGTACATGACACCCACCCAGCCCTGC	900
Qy	901	CCTGGAGCCCTGTGTACAGAGATGCTTCTTGGCCTTGCAGGTACAGTACGTGCTAGCAT	960
Db	901	CCTGGAGCCCTGTGTACAGAGATGCTTCTTGGCCTTGCAGGTACAGTACGTGCTAGCAT	960
Qy	961	GGAGTGTGAGCGCCCGGAGACGTTCCCTCTCTTCTCGGACCGTCCCGGAGCCG	1020
Db	961	GGAGTGTGAGCGCCCGGAGACGTTCCCTCTCTTCTCGGACCGTCCCGGAGCCG	1020
Qy	1021	TGTGAGTGTGAGCGCCCGGAGCTGCTGACAGGTTTGGCTGGAACTGGGTGGCCGC	1080
Db	1021	TGTGAGTGTGAGCGCCCGGAGCTGCTGACAGGTTTGGCTGGAACTGGGTGGCCGC	1080
Qy	1081	CCTGGGAGCGACGACGAGTACGGCCGAGGCTGTAGCATCTTCTCGGCCCTGGCCGC	1140
Db	1081	CCTGGGAGCGACGACGAGTACGGCCGAGGCTGTAGCATCTTCTCGGCCCTGGCCGC	1140
Qy	1141	GGCAGCGGATCTGTCATCGGCGCAGAGGCTGTGGTGGCTGCGGCTGGGATGATC	1200
Db	1141	GGCAGCGGATCTGTCATCGGCGCAGAGGCTGTGGTGGCTGCGGCTGGGATGATC	1200
Qy	1201	CGGCTGGGGAAGGTGACAGGAGCTCTGACAGGTGAACACAGCAGCGTGCAGGTTGGT	1260
Db	1201	CGGCTGGGGAAGGTGACAGGAGCTCTGACAGGTGAACACAGCAGCGTGCAGGTTGGT	1260
Qy	1261	GCTGTGTTTCTGCTCGGTGACAGGCTGACAGGCTCTTCAACTACAGCATCAGCAGCAG	1320
Db	1261	GCTGTGTTTCTGCTCGGTGACAGGCTGACAGGCTCTTCAACTACAGCATCAGCAGCAG	1320
Qy	1321	GCTCTCGCCAGGTTGGGTGGCCAGGAGGCTGGCTGACCTCTGACCTGCTGATGG	1380
Db	1321	GCTCTCGCCAGGTTGGGTGGCCAGGAGGCTGGCTGACCTCTGACCTGCTGATGG	1380
Qy	1381	GCTGCGCGCATGGCCAGATGGGCACGGTGTCTTGGCTTCTCCAGAGGGTGTCCAGCT	1440
Db	1381	GCTGCGCGCATGGCCAGATGGGCACGGTGTCTTGGCTTCTCCAGAGGGTGTCCAGCT	1440
Qy	1441	GCACGAGTTCCCTCCAGTACGTGAAGACGACCTTGGCCCTGGCCACCGCCGCTTCTG	1500
Db	1441	GCACGAGTTCCCTCCAGTACGTGAAGACGACCTTGGCCCTGGCCACCGCCGCTTCTG	1500
Qy	1501	CTCTGCCCTGGGCGAGAGGAGCAGGCTCTGGAGGAGGAGCTGTGGTGGCCAGCGCTGCC	1560
Db	1501	CTCTGCCCTGGGCGAGAGGAGCAGGCTCTGGAGGAGGAGCTGTGGTGGCCAGCGCTGCC	1560
Qy	1561	GCAGTGTGACTGCATCACGCTGCAGAACGTGAGCGAGGGCTAAATCACACAGAGCTT	1620
Db	1561	GCAGTGTGACTGCATCACGCTGCAGAACGTGAGCGAGGGCTAAATCACACAGAGCTT	1620
Qy	1621	CTCTGTCTACGAGCTGTGTATAGCGTGGCCAGGCGCTTCAACACTCTTCAGTGCAT	1680
Db	1621	CTCTGTCTACGAGCTGTGTATAGCGTGGCCAGGCGCTTCAACACTCTTCAGTGCAT	1680
Qy	1681	CGCTCAGGCTGCCCGCGCAGGACCCCGTGAAGCCCTGGCAGGTGAGCCCGGAGATGG	1740
Db	1681	CGCTCAGGCTGCCCGCGCAGGACCCCGTGAAGCCCTGGCAGGTGAGCCCGGAGATGG	1740
Qy	1741	GGGTGTGCTCTCTCTGCTATGTGCCAGGCCACAGGACCGGCCACCGCTGAGCTGG	1800
Db	1741	GGGTGTGCTCTCTCTGCTATGTGCCAGGCCACAGGACCGGCCACCGCTGAGCTGG	1800
Qy	1801	AGGTGGTGGCGGTGAGCCCGCTCCCGCCCGCGCAGCTCTTGGAGAACATGTACAACCT	1860
Db	1801	AGGTGGTGGCGGTGAGCCCGCTCCCGCCCGCGCAGCTCTTGGAGAACATGTACAACCT	1860
Qy	1861	GACCTTCCAGTGGCGGGTGGCGCTGCGCTTCCAGCAGCAGCGGAAACCTGGGACATGGA	1920
Db	1861	GACCTTCCAGTGGCGGGTGGCGCTGCGCTTCCAGCAGCAGCGGAAACCTGGGACATGGA	1920
Qy	1921	GTAACGCTTGAAGCTGTGGGTGTGGAGGCTTCACTGCGCCAGGCTTCAACGAGTGGGAG	1980
Db	1921	GTAACGCTTGAAGCTGTGGGTGTGGAGGCTTCACTGCGCCAGGCTTCAACGAGTGGGAG	1980
Qy	1981	GTTTCAACGGCAGCTCAGGACAGGCGCTTGAAGATCCGCTGGCAGACCTGTGACACCA	2040
Db	1981	GTTTCAACGGCAGCTCAGGACAGGCGCTTGAAGATCCGCTGGCAGACCTGTGACACCA	2040
Qy	2041	GTTGAGTGTGGGTGTGGGTGTGGCAGGCTGCGCCGTGAGCCCGCGGAGGGCGCAGC	2100
Db	2041	GTTGAGTGTGGGTGTGGGTGTGGCAGGCTGCGCCGTGAGCCCGCGGAGGGCGCAGC	2100
Qy	2101	CTGGGGTGGGGCCGTTCCAGTCTCCGTTGGGATGCCAGCGGATGCCAGCGAGCAGACCC	2160
Db	2101	CTGGGGTGGGGCCGTTCCAGTCTCCGTTGGGATGCCAGCGGATGCCAGCGAGCAGACCC	2160
Qy	2161	CAGGCTGTGGGAGAGCCCGTGTCCGCTGCTGCGGCGAGTCCAGGAGGGCCAGGTG	2220
Db	2161	CAGGCTGTGGGAGAGCCCGTGTCCGCTGCTGCGGCGAGTCCAGGAGGGCCAGGTG	2220
Qy	2221	CGCCGGTCAAGGGGTTCCACTCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2280
Db	2221	CGCCGGTCAAGGGGTTCCACTCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2280
Qy	2281	TACCGGCAAAACCCAGGTGAGCCCTTCCCGGAGGCGGGGTGGGAAACGACAGAGGG	2340
Db	2281	TACCGGCAAAACCCAGGTGAGCCCTTCCCGGAGGCGGGGTGGGAAACGACAGAGGG	2340
Qy	2341	AGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2400
Db	2341	AGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2400
Qy	2401	GCGCCCTTCTCTCTCTCACAGCAGCATCGCTTCTGACCTTTTGTGGCCAGGATGAGTG	2460
Db	2401	GCGCCCTTCTCTCTCTCACAGCAGCATCGCTTCTGACCTTTTGTGGCCAGGATGAGTG	2460

[illegible]

QY 661 TGGCAAGGCGAGCGCGACATCGCCGCTACTGCAACTACGCGAGTACCAGCCC 720
Db 661 TGGCAAGGCGAGCGCGACATCGCCGCTACTGCAACTACGCGAGTACCAGCCC 720
QY 721 GTGTGCTGGCTGTCTATCGGGCCCCACCTGTCAGAGCTCGCCATGTCACCGGCAAGTTCT 780
Db 721 GTGTGCTGGCTGTCTATCGGGCCCCACCTGTCAGAGCTCGCCATGTCACCGGCAAGTTCT 780
QY 781 TCAGCTTCTTCTCTCATGCCCGAGTGGGGCGCCCCCACCACATCACCCACCCCAACCAACC 840
Db 781 TCAGCTTCTTCTCTCATGCCCGAGTGGGGCGCCCCCACCACATCACCCACCCCAACCAACC 840
QY 841 CCTGCCCGTGGAGGCCCTTGTGTAGAGAAATGCTACATGACACCCACCCAGCCCTGC 900
Db 841 CCTGCCCGTGGAGGCCCTTGTGTAGAGAAATGCTACATGACACCCACCCAGCCCTGC 900
QY 901 CCTGGGAGCCTGTGTAGAGAAATGCTTGGCCCTTCAGAGTACAGTACAGTGTAGCAT 960
Db 901 CCTGGGAGCCTGTGTAGAGAAATGCTTGGCCCTTCAGAGTACAGTGTAGCAT 960
QY 961 GBAAGTCTGAGCGCCCGGAGACCTTCCCTCTCTTCTTCGCAACCGTGGCCAGCGACCG 1020
Db 961 GBAAGTCTGAGCGCCCGGAGACCTTCCCTCTCTTCTTCGCAACCGTGGCCAGCGACCG 1020
QY 1021 TGTGCACTGACCGCGCCCGGAGTGTGTGAGAGATGTCGCTGGAATGAGTGGTGGCCG 1080
Db 1021 TGTGCACTGACCGCGCCCGGAGTGTGTGAGAGATGTCGCTGGAATGAGTGGTGGCCG 1080
QY 1081 CCTGGGAGCGACGAGTACGGCGCGGAGGCTGAGCATCTTCTCGGCCCTTGGCCG 1140
Db 1081 CCTGGGAGCGACGAGTACGGCGCGGAGGCTGAGCATCTTCTCGGCCCTTGGCCG 1140
QY 1141 GGAACGCGCATCTGATCGCAACGAGGCGCTGGTCCCGCTGCCCCGTCGCCATGACTC 1200
Db 1141 GGAACGCGCATCTGATCGCAACGAGGCGCTGGTCCCGCTGCCCCGTCGCCATGACTC 1200
QY 1201 GCGGCTGGGAAAGTGCAGACGTCTGTGACACGAGTGAAACAGAGCAGCTGAGTGGT 1260
Db 1201 GCGGCTGGGAAAGTGCAGACGTCTGTGACACGAGTGAAACAGAGCAGCTGAGTGGT 1260
QY 1261 GCTGCTGTTGCGCTCGTGCACCGCGCCAGCGCTTCTTCACTACAGATCAGCAGCAG 1320
Db 1261 GCTGCTGTTGCGCTCGTGCACCGCGCCAGCGCTTCTTCACTACAGATCAGCAGCAG 1320
QY 1321 GCTCTCGCCCAAGTGTGGTGGCCAGCGAGGCTTGGTACCTCTGACCTGTGATGG 1380
Db 1321 GCTCTCGCCCAAGTGTGGTGGCCAGCGAGGCTTGGTACCTCTGACCTGTGATGG 1380
QY 1381 GCTGCCCGCATGGCCAGATGGGACGGTGTGGCTTCTCCAGAGGGTGCAGCT 1440
Db 1381 GCTGCCCGCATGGCCAGATGGGACGGTGTGGCTTCTCCAGAGGGTGCAGCT 1440
QY 1441 GCAGAGTTCCCGCAGTACGTGAAGACGACCTGGCCCTGGCCACCGACCGGCTTCTG 1500
Db 1441 GCAGAGTTCCCGCAGTACGTGAAGACGACCTGGCCCTGGCCACCGGCTTCTG 1500
QY 1501 CTCTGCCCTGGGCGAGGAGGAGCGAGGTCTGGAGGAGCGTGGTGGCGAGCGCTGCC 1560
Db 1501 CTCTGCCCTGGGCGAGGAGGAGCGAGGTCTGGAGGAGCGTGGTGGCGAGCGCTGCC 1560
QY 1561 GCAGTGTGACTGATCACCTGCAGAACGTGACGCGAGGGCTAAATCAACACAGCTT 1620
Db 1561 GCAGTGTGACTGATCACCTGCAGAACGTGACGCGAGGGCTAAATCAACACAGCTT 1620
QY 1621 CTCTGTCTACGAGCTGTGTATAGCTGTGCGCCAGGCTTGCACACACTCTTCACTGCA 1680
Db 1621 CTCTGTCTACGAGCTGTGTATAGCTGTGCGCCAGGCTTGCACACACTCTTCACTGCA 1680
QY 1681 CCGCTCAGGCTGCCCGCGCAGGACCCCGTGAAGCTTGGAGGTGAGCCGGGAGATGG 1740
Db 1681 CCGCTCAGGCTGCCCGCGCAGGACCCCGTGAAGCTTGGAGGTGAGCCGGGAGATGG 1740
QY 1741 GGGTGTGCTGCTCTCTGATGTGCCAGGCGCCAGGCGACGCCCTGAGCTGG 1800

Db 1741 GGGTGTGCTGCTCTCTGATGTGCCAGGCGCACAGGCGCACCGCTGAGCTGG 1800
QY 1801 AGTGGCTGGCGCTCAGCCCGCTCCCGCCCGCAGCTCTCTGAGAACATGTACAACCT 1860
Db 1801 AGTGGCTGGCGCTCAGCCCGCTCCCGCCCGCAGCTCTCTGAGAACATGTACAACCT 1860
QY 1861 GACCTTCCAGTGGCGGGCTGCGGCTCGAGCTTCGACAGCAGCGAAACGTGGACATGGA 1920
Db 1861 GACCTTCCAGTGGCGGGCTGCGGCTTCGACAGCAGCGAAACGTGGACATGGA 1920
QY 1921 GTACGACCTGAAGCTGTGGGTGTGGCAGGCTCAGTGCCTCAGAGCTCCACGACGTGGGCG 1980
Db 1921 GTACGACCTGAAGCTGTGGGTGTGGCAGGCTCAGTGCCTCAGAGCTCCACGACGTGGGCG 1980
QY 1981 GTTCAACGCGCAGCCTCAGGACAGAGCCTCTGAAGATCCGTGTGGCACACGTCTGACAA 2040
Db 1981 GTTCAACGCGCAGCCTCAGGACAGAGCCTCTGAAGATCCGTGTGGCACACGTCTGACAA 2040
QY 2041 GGTGAGTGTAGGCTGTGGTGTGGCAGGCTCAGTGCCTCAGAGCTCCCGCGGCGGCGCAG 2100
Db 2041 GGTGAGTGTAGGCTGTGGTGTGGCAGGCTCAGTGCCTCAGAGCTCCCGCGGCGGCGCAG 2100
QY 2101 CTGGGGGTGGGGGCGCTTCCAGTCTCCCGTGGGCTATGCCAGCGCAGCAGCAGCAGC 2160
Db 2101 CTGGGGGTGGGGGCGCTTCCAGTCTCCCGTGGGCTATGCCAGCGCAGCAGCAGCAGC 2160
QY 2161 CAGGCTGTGCGCAGAGCCTGCTCCCGTGTGCGGCGAGTCCAGAGGCGCAGGTG 2220
Db 2161 CAGGCTGTGCGCAGAGCCTGCTCCCGTGTGCGGCGAGTCCAGAGGCGCAGGTG 2220
QY 2221 CGCGGCTCAAGGGTTCACCTCTGCTGCTACAGCTGTGCTGCTGCTGCTGCTGCTGCTG 2280
Db 2221 CGCGGCTCAAGGGTTCACCTCTGCTGCTACAGCTGTGCTGCTGCTGCTGCTGCTGCTG 2280
QY 2281 TACCGGCAAAACCCAGGTGAGCGCCTTCCCGCAGCGCGGGTGGGAAACGACAGCGGG 2340
Db 2281 TACCGGCAAAACCCAGGTGAGCGCCTTCCCGCAGCGCGGGTGGGAAACGACAGCGGG 2340
QY 2341 AGGGTCTGCGCAAGTCTGACTCTGAGACAGAGCCACAGGGTACAGAGCAACACCCA 2400
Db 2341 AGGGTCTGCGCAAGTCTGACTCTGAGACAGAGCCACAGGGTACAGAGCAACACCCA 2400
QY 2401 GCGCCCTTCTCTCTCTCAGACGACATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
Db 2401 GCGCCCTTCTCTCTCTCAGACGACATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
QY 2461 TCCCGGAGCGAAGCACAGCTGCTTCCCGCGCAGGTCTCGGTTCTGCTGCTGCTGCTGCTG 2520
Db 2461 TCCCGGAGCGAAGCACAGCTGCTTCCCGCGCAGGTCTCGGTTCTGCTGCTGCTGCTGCTG 2520
QY 2521 CCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
Db 2521 CCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
QY 2581 TTGGGGCTGCTGCTTCAACCATCGGACAGCCCACTGGTTTCAGGCTCGGGGGGGCCCCCTG 2640
Db 2581 TTGGGGCTGCTGCTTCAACCATCGGACAGCCCACTGGTTTCAGGCTCGGGGGGGCCCCCTG 2640
QY 2641 GCTGCTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700
Db 2641 GCTGCTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700
QY 2701 CAGCCAGCCCTGCGCGATGCTGCGCCAGAGCGCTTGTCCCACTCCCGCTCAGCGGC 2760
Db 2701 CAGCCAGCCCTGCGCGATGCTGCGCCAGAGCGCTTGTCCCACTCCCGCTCAGCGGC 2760
QY 2761 TGCCTGAGCACACTCTTCTGTCAGGCGCGGAGATCTTCTGTCAGTCTGCTGCTGCTGCTG 2820
Db 2761 TGCCTGAGCACACTCTTCTGTCAGGCGCGGAGATCTTCTGTCAGTCTGCTGCTGCTGCTG 2820
QY 2821 AGCTGGCAGACCGCTGAGTGGCTGCTGCGGGGGCGCTGCGCTGCTGCTGCTGCTGCTGCTG 2880

2821	Db	AGCTGGCGAGACCGGCTAGTGGCTGCTCGGGGGGGCCCTGGGGCCCTGGCTGGTGGTGGCTGCTG	2888
2881	Qy	CTGGCCATGCTGGTGGAGGTGCGCACTGTGCACCTGTGTAACCTGGTGGGCTTCCCGCCGGAG	2940
2881	Db	CTGGCCATGCTGGTGGAGGTGCGCACTGTGCACCTGTGTAACCTGGTGGGCTTCCCGCCGGAG	2940
2941	Qy	GTGGTGACGAACTGGCAATGCTGTGCCACGGAGGCGCTGGTGCACTGCCGGACACGCTCC	3000
2941	Db	GTGGTGACGGAACCTGGCAATGCTGTGCCACGGAGGCGCTGGTGCACTGCCGGACACGCTCC	3000
3001	Qy	TGGGTAGCTTTCGGCCTTAGCGCAGCGCACCAATGCCACGTGGCGCTTCTCTGCTTCCCTG	3060
3001	Db	TGGGTAGCTTTCGGCCTTAGCGCAGCGCACCAATGCCACGTGGCGCTTCTCTGCTTCCCTG	3060
3061	Qy	GGCACTTTCCTGGTGGGAGCCAGCCGGGCTGTACAACCGTGGCCCTGGGCTCACCTTT	3120
3061	Db	GGCACTTTCCTGGTGGGAGCCAGCCGGGCTGTACAACCGTGGCCCTGGGCTCACCTTT	3120
3121	Qy	GCCATGCTGGCTACTTTCATGCACTGGGTCTCCTTTGTGCCCCCTCTGGGCAATGTGCAG	3180
3121	Db	GCCATGCTGGCCTACTTTCATGCACTGGGTCTCCTTTGTGCCCCCTCTGGGCAATGTGCAG	3180
3181	Qy	GTGGTCTCAGGCCCGGGTGCAGATGGGGCCCTCTCTGTGTCTCTGGGCAATCCTG	3240
3181	Db	GTGGTCTCAGGCCCGGGTGCAGATGGGGCCCTCTCTGTGTCTCTGGGCAATCCTG	3240
3241	Qy	GCTGGCTTCCACCTGCCAGGTGTACTGTCTATGGGAGCCAGAGGCTCAACACCCCC	3300
3241	Db	GCTGGCTTCCACCTGCCAGGTGTACTGTCTATGGGAGCCAGAGGCTCAACACCCCC	3300
3301	Qy	GAGTTCTTCTGGAGGGGGCCCTGGGGATGCCCAAGGCCAGAATGACGGGAAACAGGA	3360
3301	Db	GAGTTCTTCTGGAGGGGGCCCTGGGGATGCCCAAGGCCAGAATGACGGGAAACAGGA	3360
3361	Qy	AATCAGGGGAAAATGAGTGACCAACCTGTGTATCTACGCCCGGTGAACCCAGACTTA	3420
3361	Db	AATCAGGGGAAAATGAGTGACCAACCTGTGTATCTACGCCCGGTGAACCCAGACTTA	3420
3421	Qy	GCTGGCATCCCCCAAGCCAGCAAGTACCCGCTGTCTCGCTACAGAGACCTCCCGCTCT	3480
3421	Db	GCTGGCATCCCCCAAGCCAGCAAGTACCCGCTGTCTCGCTACAGAGACCTCCCGCTCT	3480
3481	Qy	AGGTTCTTGACCCCGAGTTGTCTCTGTACCCTGACCCCAACAGTGGCCCTTAGGCTGGAGC	3540
3481	Db	AGGTTCTTGACCCCGAGTTGTCTCTGTACCCTGACCCCAACAGTGGCCCTTAGGCTGGAGC	3540
3541	Qy	ACGTGGACAACCTGTGACCATC	3563
3541	Db	ACGTGGACAACCTGTGACCATC	3563

RESULT 5

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US-10-724-222-20
; Sequence 20, Application US/1072422
; Publication No. US20040191805A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: LI, XIADONG
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: STASZEWSKI, LENA
; TITLE OF INVENTION: TLR TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0277870/RXT
; CURRENT APPLICATION NUMBER: US/10/724,222
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/799,629
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: 60/187,546
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/195,536
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/209,840
; PRIOR FILING DATE: 2000-06-06

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; PRIOR APPLICATION NUMBER: 60/214,213									
; PRIOR FILING DATE: 2000-06-23									
; PRIOR APPLICATION NUMBER: 60/226,448									
; PRIOR FILING DATE: 2000-08-17									
; PRIOR APPLICATION NUMBER: 60/259,227									
; PRIOR FILING DATE: 2001-01-03									
; NUMBER OF SEQ ID NOS: 20									
; SOFTWARE: Patent In Ver. 2.1									
; SEQ ID NO 20									
; LENGTH: 3563									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-10-724-222-20									
Query Match 100.0%; Score 3563; DB 18; Length 3563;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 3563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	AGCCTGGCAGTGGCCTCAGGCAGAGTCTGACGGCGCAAAACTTTTCAGGCCACGGAAGCGA	60						
Db	1	AGCCTGGCAGTGGCCTCAGGCAGAGTCTGACGGCGCAAAACTTTTCAGGCCACGGAAGCGA	60						
QY	61	GGACACCACTGGGGCCCCAGGGTGTGCAAGTGGAGATGGCAAGGTTTTCCTAAACAAA	120						
Db	61	GGACACCACTGGGGCCCCAGGGTGTGCAAGTGGAGATGGCAAGGTTTTCCTAAACAAA	120						
QY	121	TCCTCTGCCCGCTCCCCGCCGCCGGGCTCACTCCATGTGAGGCCCCAGTCGGGGCAGGCAC	180						
Db	121	TCCTCTGCCCGCTCCCCGCCGCCGGGCTCACTCCATGTGAGGCCCCAGTCGGGGCAGGCAC	180						
QY	181	CTGCCGTGCCCTTTGGAAGTTGCCTCTGSCATGCTGGGGCCCTGCTGTCCTGGGCTCAGC	240						
Db	181	CTGCCGTGCCCTTTGGAAGTTGCCTCTGSCATGCTGGGGCCCTGCTGTCCTGGGCTCAGC	240						
QY	241	CTCTGGGGCTCTCTGCACCCCTGGGACGGGGGCCCATTTGTGCCTGTGCACAGCAACTTAGG	300						
Db	241	CTCTGGGGCTCTCTGCACCCCTGGGACGGGGGCCCATTTGTGCCTGTGCACAGCAACTTAGG	300						
QY	301	ATGAAGGGGACTACGTGTGGGGGGGCTGTTCCTCCCTGGCGCAGGCCGAGGAGGCTGGC	360						
Db	301	ATGAAGGGGACTACGTGTGGGGGGGCTGTTCCTCCCTGGCGCAGGCCGAGGAGGCTGGC	360						
QY	361	CTCCGACGCCGACACGGCCCGCAGCCCTGTGTGACACAGGTACAGAGTGGGACGGCC	420						
Db	361	CTCCGACGCCGACACGGCCCGCAGCCCTGTGTGACACAGGTACAGAGTGGGACGGCC	420						
QY	421	TGGGTCCGGGTACAGGTGTGGGGTGTCTCTGAGCTTGGGGCCGAGGTGGCCAT	480						
Db	421	TGGGTCCGGGTACAGGTGTGGGGTGTCTCTGAGCTTGGGGCCGAGGTGGCCAT	480						
QY	481	CTGGGTTCCTGTGTGGCCCGCAGGTTCTCTCAACAGCCCTGCTCTGGGCACTGGCCATGA	540						
Db	481	CTGGGTTCCTGTGTGGCCCGCAGGTTCTCTCAACAGCCCTGCTCTGGGCACTGGCCATGA	540						
QY	541	AAATPGCCGTGGAGGAGATCAACAAAGTCGATCTGTCTGCCCGGCTCGCGCTGGGCT	600						
Db	541	AAATPGCCGTGGAGGAGATCAACAAAGTCGATCTGTCTGCCCGGCTCGCGCTGGGCT	600						
QY	601	ACGACCTCTTTGATACGTGTCTCGAGGCTGTGGTGGCCATGAAGCCGAGCTCATGTTCC	660						
Db	601	ACGACCTCTTTGATACGTGTCTCGAGGCTGTGGTGGCCATGAAGCCGAGCTCATGTTCC	660						
QY	661	TGGCCAAGGCAGGCAGCCGCGCATCGCCGCTACTGCAACTACACGCAGTACCGACCCC	720						
Db	661	TGGCCAAGGCAGGCAGCCGCGCATCGCCGCTACTGCAACTACACGCAGTACCGACCCC	720						
QY	721	GTGTGCTGGCTGTATCGGGCCCCACTCGTTCAGAGTCTCGCATGTGTACCGGCAAGTTCT	780						
Db	721	GTGTGCTGGCTGTATCGGGCCCCACTCGTTCAGAGTCTCGCATGTGTACCGGCAAGTTCT	780						
QY	781	TCAGCTCTTCTCATGCCCGCCAGTGGGGGCCCCCCCATCATACCCACCCCAACCAACC	840						
Db	781	TCAGCTCTTCTCATGCCCGCCAGTGGGGGCCCCCCCATCATACCCACCCCAACCAACC	840						

[illegible]


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Db 3001 TGGGTGAGTTCGGCTAGCGACGCCACCAATGCCAGCTGCGCTTCTCTGCTTCTG 3060
Qy 3061 GGCACATTTCTGCTGCGGAGCAGCGGGTGTGTACAAACGTCGCGTGGCCCTCACCTTT 3120
Db 3061 GGCACATTTCTGCTGCGGAGCAGCGGGTGTGTACAAACGTCGCGTGGCCCTCACCTTT 3120
Qy 3121 GCATGCTGGCTTACTTCACTACCTGGGTCTCTTTGTGGCCCTCTCTGGCCAAATGTGCAG 3180
Db 3121 GCCATGCTGGCTTACTTCACTACCTGGGTCTCTTTGTGGCCCTCTCTGGCCAAATGTGCAG 3180
Qy 3181 GTGGTCTCAGGCCCGCGTGCAGATGGGGCGCCCTCTGCTCTGTGTCTTGGGATCCTG 3240
Db 3181 GTGGTCTCAGGCCCGCGTGCAGATGGGGCGCCCTCTGCTCTGTGTCTTGGGATCCTG 3240
Qy 3241 GGTGCTCTCCACCTGCGCCAGGTGTACCTGCTCATGCGGAGCAGGGCTCAACACCC 3300
Db 3241 GGTGCTCTCCACCTGCGCCAGGTGTACCTGCTCATGCGGAGCAGGGCTCAACACCC 3300
Qy 3301 GAGTTCTTCTGGAGGGGGCCCTGGGGATGCCAAAGGCCAGATGACGGGAACACAGGA 3360
Db 3301 GAGTTCTTCTGGAGGGGGCCCTGGGGATGCCAAAGGCCAGATGACGGGAACACAGGA 3360
Qy 3361 AATCAGGGGAACATGAGTACCCACCTGTGATCTCAGCCCGGTGAACCCAGACTTA 3420
Db 3361 AATCAGGGGAACATGAGTACCCACCTGTGATCTCAGCCCGGTGAACCCAGACTTA 3420
Qy 3421 GGTGCTATCCCCCCCCAAGCAGCAATGACCCGTTGATGCCAAAGGCCAGATGACGGGAACACAGGA 3480
Db 3421 GGTGCTATCCCCCCCCAAGCAGCAATGACCCGTTGATGCCAAAGGCCAGATGACGGGAACACAGGA 3480
Qy 3481 AGTTCTGACCCCGAGTTGTCTCTGACCCCTGACCCAGTGAAGCCCTAGGCTGGAGC 3540
Db 3481 AGTTCTGACCCCGAGTTGTCTCTGACCCCTGACCCAGTGAAGCCCTAGGCTGGAGC 3540
Qy 3541 ACGTGACACCCCTGTGACCATC 3563
Db 3541 ACGTGACACCCCTGTGACCATC 3563
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RESULT 6

US-10-725-276-20

; Sequence 20, Application US/10725276

; Publication No. US20040209286A1

; GENERAL INFORMATION:

; APPLICANT: ADLER, JON ELLIOT

; APPLICANT: LI, XIAODONG

; APPLICANT: STASZEWSKI, LENA

; APPLICANT: O'CONNELL, SHAWN

; APPLICANT: ZOZULYA, SERGEY

; TITLE OF INVENTION: TLR TASTE RECEPTORS AND GENES ENCODING SAME

; FILE REFERENCE: 078003-0280681

; CURRENT APPLICATION NUMBER: US/10/725,276

; CURRENT FILING DATE: 2003-12-02

; PRIOR APPLICATION NUMBER: 60/259,227

; PRIOR FILING DATE: 2001-01-03

; PRIOR APPLICATION NUMBER: 60/284,547

; PRIOR FILING DATE: 2001-04-19

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20

; LENGTH: 3563

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-725-276-20

Query Match

Best Local Similarity 100.0%; Score 3563; DB 18; Length 3563;

Matches 3563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCTGGCAGTGGCTCTAGGCGAGTCTGACCGGCACAACTTTAGGCCACGAGGCGA 60

Db 1 AGCCTGGCAGTGGCTCTAGGCGAGTCTGACCGGCACAACTTTAGGCCACGAGGCGA 60

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 1141 GGCACGGGATCTGATCGGACAGAGGCTGTCGCGTGCCTGCGGATGACTC 1200
 1201 GCGGCTGGGAAGTGCAGGACGTCCTGACAGAGTGAACAGAGCAGCGTGAGTGGT 1260
 1201 GCGGCTGGGAAGTGCAGGACGTCCTGACAGAGTGAACAGAGCAGCGTGAGTGGT 1260
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 1321 GCTGCTGTCGCTCCGTCGACGCGCCACGCGCTCTTCACTACAGCATCAGCAGCAG 1380
 1381 GCTGCTGTCGCTCCGTCGACGCGCCACGCGCTCTTCACTACAGCATCAGCAGCAG 1440
 1381 GCTGCTGTCGCTCCGTCGACGCGCCACGCGCTCTTCACTACAGCATCAGCAGCAG 1440
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 1441 GACAGAGTTCCTCCAGTACGTAAGACGACCTGCGCTGCGCCACGCGCGCTCTCTG 1500
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 1501 CTCTGCTGCGGCGAGAGGAGCAGGCTCTGAGAGGACCTGCTGCGCCACGCGCGCTCTG 1560
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 1561 GCAGTGTGACTGCTACGCTGACAGACGTCGAGCGCAGGCTAAATACACACGACGCTT 1620
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 1621 CTCTGCTACGAGCTGTATAGGCTGCGCCAGGCTGCTGAGAGGACCTCTCTGAGTCAA 1680
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 1681 GCGCTCAGGCTGCGCGCGCAGAGCCTGCTGAGAGCCTGCGAGGCTGAGCGCGGAGATGG 1740
 1741 GGGTGTGCTGCTCTGATGTCGCGGACAGGACAGGCGCAGGCTGAGCTGAGCTGG 1800
 1741 GGGTGTGCTGCTCTGATGTCGCGGACAGGACAGGCGCAGGCTGAGCTGAGCTGG 1800
 1801 AGGTGGCTGGCGCTCAGCGCGCTGCGCGCGCAGCTCTGAGAGACATGTAACCT 1860
 1801 AGGTGGCTGGCGCTCAGCGCGCTGCGCGCGCAGCTCTGAGAGACATGTAACCT 1860
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 1921 GTACGACCTGAAGCTGTGGGTGTGGAGGCTGAGCTGAGCTGAGCTGAGCTGG 1980
 1921 GTACGACCTGAAGCTGTGGGTGTGGAGGCTGAGCTGAGCTGAGCTGAGCTGG 1980
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2221 CCGCGGGTCAAGGGGTTCACCTCTGCTGTGCTACGACTGTGTGAGCTGTGAGCTGTGAGCTGTGAGCT 2280
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 2281 TACCGGCAAAACCCAGGTGAGCGCTTCCGCGAGCGCGGGTGGGAAACGACAGAGGG 2340
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 2341 AGGTCCTGCAAGTCTGACTCTGAGACAGAGCCCAACAGGCTACAGAGCAACACCCA 2400
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 2461 TCCCGGAGCGAGACACGCTGCTCCGCGAGAGTCTCGGTCCTGAGCATGCGGCGAG 2520
 2461 TCCCGGAGCGAGACACGCTGCTCCGCGAGAGTCTCGGTCCTGAGCATGCGGCGAG 2520
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 2521 CCGGCTGTGCTGCTGCTCTGCTGCTGAGCCTGCGCTGCGGCTGCTGCTGCTGCTGCTGCT 2580
 2581 TTGGGGCTGTGCTTCAACATCGGACAGCCCACTGCTTCAAGGCTCGGGGGGCGCCCTG 2640
 2581 TTGGGGCTGTGCTTCAACATCGGACAGCCCACTGCTTCAAGGCTCGGGGGGCGCCCTG 2640
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 2641 GCTGCTTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700
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 2701 CAGCCAGCCCTGCGCGATGCTGCGCCAGCAGCAGCCTTGTCCCACTCCCGCTCACGGG 2760
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 2941 GTGGTACGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
 3001 TGGGTACGCTTTCGGCTAGCGCACCGCCCAACCAATGCGCTGCGCTTCTGCTGCTGCTGCTGCTG 3060
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 3121 GGCATGCT 3180
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 3181 GTGGTCTCTCAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3240
 3241 GCTGCTCTTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3300
 3241 GCTGCTCTTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3300
 3301 GAGTCTTCTTCTGCGGAGGGGCGCTGCGGATGCGCCAGGCGCAATGACGGGAAACACAGCA 3360

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QY	3361	AATCAGGGGAAACATGAGTGACCCAAACCTCTGATCTCAGCCCCGGTGAAACCCAGACTTA	3420	
DB	3361	AATCAGGGGAAACATGAGTGACCCAAACCTCTGATCTCAGCCCCGGTGAAACCCAGACTTA	3420	
QY	3421	GCTCGGATCCCCCAGCCAGCAGCAATGACCGTGTCTCGTTACAGAGACCGCTCCCGTCT	3480	
DB	3421	GCTCGGATCCCCCAGCCAGCAGCAATGACCGTGTCTCGTTACAGAGACCGCTCCCGTCT	3480	
QY	3481	AGGTTCTGACCCACCGAGTTGTCTCTCTGACCCCTGACCCACAGTGAAGCCCTAGGCGCTGGAGC	3540	
DB	3481	AGGTTCTGACCCACCGAGTTGTCTCTCTGACCCCTGACCCACAGTGAAGCCCTAGGCGCTGGAGC	3540	
QY	3541	ACGTGGACACCCCTGTGACCATC	3563	
DB	3541	ACGTGGACACCCCTGTGACCATC	3563	

RESULT 7

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US-10-726-568-20
; Sequence 20, Application US/10726568
; Publication No. US2004022939A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: LI, XIADONG
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: STASZEWSKI, LENA
; TITLE OF INVENTION: TIR TASTE RECEPTORS AND GENES ENCODING SAME

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	Query Match	100.0%;	Score 3563;	DB 18;	Length 3563;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 3563;	Conservative	0;	Mismatches	0;
				Indels	Gaps
QY	1	AGCCTGGCAGTGGCCTCAGGCAGAGTCTGACGGCACAACATTTCAGGCCCGCAGAGCGGA	60		
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QY	61	GGACACACTGGGGGCCCCAGGGTGTGGCAAGTGAGGATGGCAAGGTTTGTCTAAACAAA	120		
Db	61	GGACACCACTGGGGGCCCCAGGGTGTGGCAAGTGAGGATGGCAAGGTTTGTCTAAACAAA	120		
QY	121	TCCTCTGCCCGCTCCCGCCGCCCGGGCTCACTCCATGTGAGGCCCCAGTCGGGGCAGGCCAC	180		
Db	121	TCCTCTGCCCGCTCCCGCCGCCCGGGCTCACTCCATGTGAGGCCCCAGTCGGGGCAGGCCAC	180		
QY	181	CTGCGCTGCTGTGGAGTTGGAGTTGCCTCTGGCCATGCTGGGCCCTGTGTCCTGGGGCTCAGC	240		
Db	181	CTGCGCTGCTGTGGAGTTGGAGTTGCCTCTGGCCATGCTGGGCCCTGTGTCCTGGGGCTCAGC	240		

1321	Db		GCTCTCGCCCAAGGTGTGGGTGGCCAGCGAGGCTTGCTGACCTTGACTGGTCATGGG	1380
1381	Qy		GCTGCCCGGCATGGCCAGATGGGCACGGTGTGGCTTCTCCACAGAGGGTGCCAGCT	1440
1381	Db		GCTGCCCGGCATGGCCAGATGGGCACGGTGTGGCTTCTCCACAGAGGGTGCCAGCT	1440
1441	Qy		GCACGAGTTTCCCGACGATGATGAAGACGACACTTGGCCCTGGCCACCGACCCGGCTTCG	1500
1441	Db		GCACGAGTTTCCCGACGATGATGAAGACGACACTTGGCCCTGGCCACCGACCCGGCTTCG	1500
1501	Qy		CTCTGCCCTGGCGAGAGGGAGCAGGGTCTGAGAGAGAGCTGGTGGCGAGCGCTGCC	1560
1501	Db		CTCTGCCCTGGCGAGAGGGAGCAGGGTCTGAGAGAGAGCTGGTGGCGAGCGCTGCC	1560
1561	Qy		GCAGTGTGACTGCACTCACGCTTGACAGACGTGAGCGCAGGGCTAAATCACACACAGAGTT	1620
1561	Db		GCAGTGTGACTGCACTCACGCTTGACAGACGTGAGCGCAGGGCTAAATCACACACAGAGTT	1620
1621	Qy		CTCTGTCTACGACGCTGTATAGCTGGCGCAGGCCCTGCACAACTCTTCAAGTGCAA	1680
1621	Db		CTCTGTCTACGACGCTGTATAGCTGGCGCAGGCCCTGCACAACTCTTCAAGTGCAA	1680
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1681	Db		CGCCTCAGGCTGCCCGCGAGGACCCGCTGAAGCCCTGGCAGGTGAGCCCGGAGATGG	1740
1741	Qy		GGGTGTGCTGCTCTGATGTGCCAGGCGCACAGGACAGGCGCACGCCCTGAGCTGG	1800
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1801	Db		AGGTGGCTGGCGGTCAAGCCCGTCCCGCGCGAGGCTCTGAGAAACATGTACAACCT	1860
1861	Qy		GACCTTCAAGTGGCGGGTGCCTGCGCTCGAGTGCAGACAGCGGAAACGTGGACATGGA	1920
1861	Db		GACCTTCAAGTGGCGGGTGCCTGCGCTCGAGTGCAGACAGCGGAAACGTGGACATGGA	1920
1921	Qy		GTACGACCTGAAGCTGTGGGTGTGGCAGGGCTCAGTGCCAGGCTCCAAGCTGGGCGAG	1980
1921	Db		GTACGACCTGAAGCTGTGGGTGTGGCAGGGCTCAGTGCCAGGCTCCAAGCTGGGCGAG	1980
1981	Qy		GTTCACCGGACGCTTCAGGACAGAGCGGCTGAAGATCGCTGGCACAGCTTCACACCA	2040
1981	Db		GTTCACCGGACGCTTCAGGACAGAGCGGCTGAAGATCGCTGGCACAGCTTCACACCA	2040
2041	Qy		GGTGAGGTGAGGGTGGGTGTGCGAGGCGTGCCTGGTGTAGCCCGCGGACGGCGAGC	2100
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2101	Qy		CTGGGGGTGGGGCGGTTCCAGTCTCCCGTGGGATGCCCAGCCGAGCAGAGCCAGACCC	2160
2101	Db		CTGGGGGTGGGGCGGTTCCAGTCTCCCGTGGGATGCCCAGCCGAGCAGAGCCAGACCC	2160
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2161	Db		CAGGCTGTGCGCAGAAAGCCCGTGTCCCGGTGCTCGCGGCAGTGCAGAGGGCGCAGGTG	2220
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2281	Db		TACCGGCAAAACCCAGGTGAGCGGCTTCCCGCAGGCGGGGTGGGAAACGACAGGGG	2340
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2341	Db		AGGGTCTGCAAGTCTGACTGTGAGACAGAGCCACAGGGTACAGAGCAACACCA	2400
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3656 AGGTGGCTGGCGCTCAGCCCGCTGAGCCCGCTGAGTGGAGTGGAGTGGAGTGG 3715
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3716 GACCTTCCAGTGGCGGCTGCGCTGCGGTTCGACAGAGCGGAAAGTGGACATGGA 3775
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3776 GTACGACTGAAGCTGTGGGTGTGGCAGGCTCAGTGGCCAGGCTCCACGACGTGGGAG 3835
1981 GTTCAAAGGAGCTCAGGACAGAGCGCTGAGATCGCTGGCACAGCTCTGACACCA 2040
3836 GTTCAAAGGAGCTCAGGACAGAGCGCTGAGATCGCTGGCACAGCTCTGACACCA 3895
2041 GGTGAGGTGAGGTGGGTGTGCGCAGGCTGCGGTGAGTGGCCCGCGGCGAGGCGCAGC 2100
3896 GGTGAGGTGAGGTGGGTGTGCGCAGGCTGCGGTGAGTGGCCCGCGGCGAGGCGCAGC 3955
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3956 CTGGGGGTGGGGCGCTTCCAGTCTCCCGTGGGATGCCAGCGGAGCAGAGCCAGCCC 4015
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4016 CAGGCTGTGGCGAAGCCCGTGTCCCGTGGTGTGCGGCGAGTGGCGAGGCGGCGAGTG 4075
2221 CGCGGGGTCAAGGGGTTCACCTCTGCTGTACGACTGTGTGAGTGGCGAGGCGGCGAGC 2280
4076 CGCGGGGTCAAGGGGTTCACCTCTGCTGTACGACTGTGTGAGTGGCGAGGCGGCGAGC 4135
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4136 TACCGGGCAAAACCCAGGTGAGCGCGCTTCCCGCAGGCGGGGTGGGAAACGAGCAGGGG 4195
2341 AGGGTCTGGCAAGTCTGACTCTGAGACAGAGCCGACAGGTTACAGACCAACACCCA 2400
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2701 CAGCCAGGCTTCCCGGATGCTGCGCCAGAGCCCTTGTCCACCTCCCGCTCAGCGGC 2760
4556 CAGCCAGGCTTCCCGGATGCTGCGCCAGAGCCCTTGTCCACCTCCCGCTCAGCGGC 4615
2761 TGCCTGAGCACACTCTTCTGCGAGGCGGCGGAGATCTTCTGAGGATCAGAACTGCCTCTG 2820

4616 TGCTGAGCACACTTCTTCTGAGGCGGCGAGATCTTCTGAGTCAAGATCTGCTCTG 4675
2821 AGCTGGGCGAGCGGCTGAGTGGCTGCTGCGGGGGCCCTTGGGCTTGGTGGTCTG 2880
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RESULT 9

US-10-292-798-601
; Sequence 601, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIHO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292, 798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 601
LENGTH: 4256

TYPE: DNA

ORGANISM: Homo sapiens

FEATURES:

LOCATION: source

FEATURE:

LOCATION: (1)..(4256)

FEATURE:

NAME/KEY: CDS

LOCATION: (201)..(391)

FEATURE:

NAME/KEY: CDS

LOCATION: (493)..(793)

FEATURE:

NAME/KEY: CDS

LOCATION: (879)..(1661)

FEATURE:

NAME/KEY: CDS

LOCATION: (1776)..(1979)

FEATURE:

NAME/KEY: CDS

LOCATION: (2114)..(2234)

FEATURE:

NAME/KEY: CDS

LOCATION: (2361)..(3315)

FEATURE:

NAME/KEY: CDS

LOCATION: (3713)..(3890)

FEATURE:

NAME/KEY: CDS

LOCATION: (3979)..(4056)

US-10-292-798-601

Query Match
Best Local Similarity 95.4%; Score 3398.6; DB 15; Length 4256;
Matches 3482; Conservative 0; Mismatches 19; Indels 52; Gaps 2;

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QY	71	GGGGCCCCAGGGTGTGGCAAGTGAAGTGGCAAGGGTTTTGCTAAACAATCTCTGCC	130
DB	61	GGGGCCCCAGGGTGTGGCAAGTGAAGTGGCAAGGGTTTTGCTAAACAATCTCTGCC	120
QY	131	GCTCCCGCCCGGGCTCACTCCATGTGAGGCCCCAGTGGGGGAGCCACTGCCGTGCC	190
DB	121	GCTCCCGCCCGGGCTCACTCCATGTGAGGCCCCAGTGGGGGAGCCACTGCCGTGCC	180
QY	191	TGTTGGAAAGTTGCCCTCTGCATGTGGGCGCTGCTGCTGGGCTCAGCCTCTGGGTC	250
DB	181	TGTTGGAAAGTTGCCCTCTGCATGTGGGCGCTGCTGCTGGGCTCAGCCTCTGGGTC	240
QY	251	TCCTGCACCTTGGACGGGGCCCCATTGTGCTGTCTCAGCAAATTAGGATGAAGGGG	310
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QY	371	GGACAGGCCAGCAGCCTGTGTGTCACAGGTACAGAGGTGGAGCGCCTGGGTGGGG	430
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QY	431	TCAGGGTGAACAGGTCTGGGGTGTCTCTGAGTGGGGCCGAGGTGGCCATCTGGGTTCT	490
DB	421	TCAGGGTGAACAGGTCTGGGGTGTCTCTGAGTGGGGCCGAGGTGGCCATCTGGGTTCT	480
QY	491	GTGTGGCCCCAGGTCTCTCTCAAGGGCTGTCTGGGCACTGGGCCATGAATGGCCGT	550

DB	481	GTGTGGCCCCAGGTCTCTCTCAAGCGCCTGCTCTGGGCACTGGCCATGAATGGCCGT	540
QY	551	GGAGGAGATCAACAACAAGTCGGATCTGCTCCCGGGCTGCGCTGGGCTACGACCTCTT	610
DB	541	GGAGGAGATCAACAACAAGTCGGATCTGCTCCCGGGCTGCGCTGGGCTACGACCTCTT	600
QY	611	TGATACGTCTGGAGCCTGTGTGGCCATGAAGCCAGCCTCATGTTCTTGGCCAAAGGC	670
DB	601	TGATACGTCTGGAGCCTGTGTGGCCATGAAGCCAGCCTCATGTTCTTGGCCAAAGGC	660
QY	671	AGGAGCGCGGACATCGCCGCTTACTGCAACTACGCACTACGAGCGCGTGTGCTGGC	730
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DB	721	TGTATCGGGCCCCACTCGTCAGAGCTCGCATGGTCACCGGCAAGTTCTTCAAGCTTCTT	780
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DB	781	CCTATGCCCCAGTGGGGGCCCCCAACATCAACCAACCCCAACCAACCCCTGCCCCGT	840
QY	851	GGGAGCCCCCTTGTGTGTCAGGAGATGCTACATGACACCCCAACCCCTGCCCCGTGGAGCC	910
DB	841	GAG---CCCTGTGTGTCAGGAGATGCT-----	864
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QY	971	AGGCGCCGGAGACCTTCCCTCTTCTTCCGACCGTCCCGACCGTGTGCAAGCTG	1030
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QY	1031	AGGCGCCGGAGACCTTCTGAGGAGTTCGGGTGAACTGGGTGCGCCCTGCGGACG	1090
DB	969	AGGCGCCGGAGACCTTCTGAGGAGTTCGGGTGAACTGGGTGCGCCCTGCGGACG	1028
QY	1091	GACGACGAGTACGGCGCGGAGGCTGAGCATCTTCTCGGCCCTGCGCCGCGGACGCGGC	1150
DB	1029	GACGACGAGTACGGCGCGGAGGCTGAGCATCTTCTCGGCCCTGCGCCGCGGACGCGGC	1088
QY	1151	ATCTGCATCGCCACGAGGCTGTGTGCGCTGTGCGCTGTGCGCTGTGCGCTGTGCGG	1210
DB	1089	ATCTGCATCGCCACGAGGCTGTGTGCGCTGTGCGCTGTGCGCTGTGCGCTGTGCGG	1148
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QY	1451	CCCCAGTACGTGAAGACGACCTTGGCCCTTGGCCACCGACCGGCTTCTGCTGCTGCTG	1510
DB	1389	CCCCAGTACGTGAAGACGACCTTGGCCCTTGGCCACCGACCGGCTTCTGCTGCTGCTG	1448
QY	1511	GGCAGAGGAGGAGGCTGTGGAGGAGAGCTGTGTGGGCCAGCGCTGCCAGTGTGAC	1570
DB	1449	GGCAGAGGAGGAGGCTGTGGAGGAGAGCTGTGTGGGCCAGCGCTGCCAGTGTGAC	1508
QY	1571	TGCATCAGCTGCAAGAGCTGAGCGGAGGCTTAATCACCACAGAGTCTCTGTCTAC	1630


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/ CURRENT APPLICATION NUMBER: US/10/017,161
/ CURRENT FILING DATE: 2002-12-18
/ PRIOR APPLICATION NUMBER: JP 2001/246789
/ PRIOR FILING DATE: 2001-06-18
/ NUMBER OF SEQ ID NOS: 2430
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 689
/ LENGTH: 7084
/ TYPE: DNA
/ ORGANISM: Homo sapiens
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Query Match          94.1%; Score 3354.2; DB 15; Length 7084;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 3484; Conservative 0; Mismatches 23; Indels 56; Gaps 6;

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Db 1501 AGCCTGGCAGTGGCTCAGGACAGTCTGACGGCACAACCTTCAGGCCACAGGAAGCGA 1560

QY 61 GGACACCACTGGGGCCCGAGGCTGGCAAGTGGAGATGGCAAGGTTTGTGAACAAA 120
Db 1561 GGACACCACTGGGGCCCGAGGCTGGCAAGTGGAGATGGCAAGGTTTGTGAACAAA 1620

QY 121 TCCTGTGCCGCTCCCGCCCGGCGTCACTCATGTGAGGCCCGCAGTGGGGCAGCCAC 180
Db 1621 TCCTGTGCCGCTCCCGCCCGGCGTCACTCATGTGAGGCCCGCAGTGGGGCAGCCAC 1680

QY 181 CTGCCGTGCTGTTGGAAAGTTGCCCTTGCATGCTGGGCGCTGCTGCTGGGCGCTCAGC 240
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QY 301 ATGAAGGGGACTACGTCTGGGGGGGCTGTTCCCTCCCTGGGCGAGGCGGAGGCTGGC 360
Db 1801 ATGAAGGGGACTACGTCTGGGGGGGCTGTTCCCTCCCTGGGCGAGGCGGAGGCTGGC 1860

QY 361 CTCCGAGCCGGACACGGCCACAGCCCTGTGTGACACAGGTACAGAGTGGGACGGCC 420
Db 1861 CTCCGAGCCGGACACGGCCACAGCCCTGTGTGACACAGGTACAGAGTGGGACGGCC 1920

QY 421 TGGGTGGGGTCAAGGTGACAGGTCTGGGGTGTCTCTGAGCTGGGGCCGAGGTGGCAT 480
Db 1921 TGGGTGGGGTCAAGGTGACAGGTCTGGGGTGTCTCTGAGCTGGGGCCGAGGTGGCAT 1980

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QY 541 AAATGCCGTGGAGGAGATCAACAAAGTCGGATCTGTGCCCGGGCTCGGCTGGGCT 600
Db 2041 AAATGCCGTGGAGGAGATCAACAAAGTCGGATCTGTGCCCGGGCTCGGCTGGGCT 2100

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Qy	2665	GGCTGTGTCTGCTCAGCGTCTCTGTTTCCCTGGCCAGCCGACGCGCTGCCGATGCCCTG	2724
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Qy	3085	CGGGGTGTCAAAACGCTGCGGTGGCCCTCACTTTGCCATGCTGGCTTACTTATCACC	3144
Db	2888	CGGGGTGTCAAAACGCTGCGGTGGCCCTCACTTTGCCATGCTGGCTTACTTATCACC	2947
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Qy	3205	ATGGGCGCCCTCTGCTGTGTCTCTGGGCAATCTTGGCTGCTGCTTCCAGTCCAGGTGT	3264
Db	3008	ATGGGCGCCCTCTGCTGTGTCTCTGGGCAATCTTGGCTGCTGCTTCCAGTCCAGGTGT	3067

QY	3265	TACTCTGTCATCGCGCAGCCAGGGCTCAACACCCCCGAGTCTTCTCTGGAGGGGGCCCT	3322
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RESULT 13

US-10-225-567A-592

; Sequence 592, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burner, Glenn C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 592

; LENGTH: 3115

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-225-567A-592

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	Matches 3094;	Conservative 0;			Gaps 6
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QY	331	TTCCCCCTGGGCGAGCCGAGAGGCTGGCTCCGACCCGGAACACGGCCACAGCAGCCCT	390		
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; Publication No. US2003005448A1
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; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: LI, XIADONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: T1R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003-0280681
; CURRENT APPLICATION NUMBER: US/10/035, 045
; CURRENT FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: 60/259, 227
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 60/284, 547
; PRIOR FILING DATE: 2001-04-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2687
; TYPE: DNA
; ORGANISM: Homo sapiens
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Title: US-10-035-045-21

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Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1

US-09-361-631-7

; Sequence 7, Application US/09361631

; Patent No. 6383778

; GENERAL INFORMATION:

; APPLICANT: Zuker, Charles S.

; APPLICANT: Adler, Jon Elliot

; APPLICANT: Lindemeyer, Juergen

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor

; TITLE OF INVENTION: Involved in Sensory Transduction

; FILE REFERENCE: 02307E-0887200S

; CURRENT APPLICATION NUMBER: US/09361,631

; CURRENT FILING DATE: 1999-07-27

; EARLIER APPLICATION NUMBER: US 60/095,464

; EARLIER FILING DATE: 1998-07-28

; EARLIER APPLICATION NUMBER: US 60/112,747

; EARLIER FILING DATE: 1998-12-17

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 669

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: human G-protein coupled receptor (GPCR) B4 amino

; OTHER INFORMATION: acid sequence

US-09-361-631-7

Query Match 78.0%; Score 3463.5; DB 3; Length 669;

Best Local Similarity 97.5%; Pred. No. 0;

Matches 661; Conservative 1; Mismatches 7; Indels 9; Gaps 3;

QY	162	ITYSAISDELDRKVPFALLTTPSADHVEAMVQLMHLFRNWIIVLVSSDYGRDNGQ	221
Db	1	ITYSAISDELDRKVPFALLTTPSADHVEAMVQLMHLFRNWIIVLVSSDYGRDNGQ	60
QY	222	LLGERVARDICIAFOETPLTPQNOMTSEEROLVTIVDKLOQSTARVVVVFSPDRTL	281
Db	61	LLGERVARDICIAFOETPLTPQNOMTSEEROLVTIVDKLOQSTARVVVVFSPDRTL	120
QY	282	YHFFNEVLQRNFTGAVWTASESWAIDPVLHNLTELGLHGLTGLGITIQSVPIPGSEFREW	341
Db	121	YHFFNEVLQRNFTGAVWTASESWAIDPVLHNLTELGLHGLTGLGITIQSVPIPGSEFREW	180
QY	342	GPQAGPPPLSTSSQSYTCNQCDNCLNATLNFNTILRSGERVVYVSVYAVAAHLHS	401
Db	181	GPQAGPPPLSTSSQSYTCNQCDNCLNATLNFNTILRSGERVVYVSVYAVAAHLHS	240
QY	402	LLGCDKSTCTKRVVYVPMQLLEEIKWVNFLLDHQIFDPDQGDVALHLEIVQWQDRSQNP	461

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118 EDNLLPQEDSYNISRVAVIGPDNSSEVMTVANFLSLFLPQITVSAISDELDRKVF 177
121 DDDLLPLKDYQSYMPHVAVIGPDNSSEAITVSNILSHFLIPQITVSAISDLKDRKH 180
178 PALLRTTPSADHVEAMVQLMLHFRNWIIVLVSSDTYGRDNGQLLGERVAR-RDICIAP 236
181 PSLMLRTVPFSATHIEAMVQLMVHFQNMWIVLVSDDDYGRSHLSORLTKTSDICIAP 240
237 QETLPTLPONNMTSEBORLVTIVDKLOOSTARVVVFPSPDLTLVHFFNEVLRFQNTGA 296
241 QEVLPPESSQVMSRSEORQDNLILKRLTSARVVVFPSPDLTLVHFFNEVLRFQNTGA 300
297 VWIASEWAIDPVLHNLTELGHITGFLGIIQSVIPDGPSEFEMWQAGPPPLSRSTSQS 356
301 VWIASEWAIDPVLHNLTELGHITGFLGIIQSVIPDGPSEFEMWQAGPPPLSRSTSQS 360
357 YTCNOECDNCLNATLSFNTILRLSGERVYVSVYAVAHALHSLGCDKSTCTKVVY 416
361 TTCNQDCDACINTTKSFNNILILSGERVYVSVYAVAHALHSLGCDKSTCTKVVY 420
417 PWOLLEIWKVNFLLDHOIFPDQGDVALHLEIVQWDRSQNPFOVSASYYPLOQLK 476
421 PWOLLEIWKVNFLLDHOIFPDQGDVALHLEIVQWDRSQNPFOVSASYYPLOQLK 480
477 NIQDISMHTVNTIPMSMCKRQSGQKQKPVGHVCCFECIDCLPOTFLNHTDEYECQ 536
481 YINNVSMTVNTIPMSMCKRQSGQKQKPVGHVCCFECIDCLPOTFLNHTDEYECQ 540
537 ACPNNEWSYQSETSCPKQLVFLWEHAPTAVALAALGLFLSTLAILVFWRHFOPIV 596
541 SCPSGMSWYKNDITCFORRPTFLEWHEVPTIVAILAALGLFLSTLAILVFWRHFOPIV 600
597 RSAGGPMCFMLTLVLVAVYVVPVYVGPVKYSTCLCRQALFPLCTICISIAVRSFQIV 656
601 RSAGGPMCFMLTLVLVAVYVVPVYVGPVKYSTCLCRQALFPLCTICISIAVRSFQIV 660
657 CAFKMASRFPRAYSYVRYQGVYVMAFIVLKMVIVIGMATGLSPTTRTDDDDPKIT 716
661 CVFKMARLPSAYSFMRYHGPYVFAITAKVALVGNMATTINPIGTDDDDPNIM 720
717 IVSCNPNRSLNLTSLDILLVSVGFSAVMGKELPTNYNEAKFITLSMTFYFTSSVSL 776
721 ILSCHPNRGLNLTSLDILLVSVGFSAVMGKELPTNYNEAKFITLSMTFYFTSSVSL 780
777 CTMFSAYSGVLVTIVDILLVNLALSLGFGPKCYMILFYPERNTPAYFNSMIQGYTM 836
781 CTMFSAYSGVLVTIVDILLVNLALSLGFGPKCYMILFYPERNTPAYFNSMIQGYTM 840
837 RR 838
841 RK 842

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RESULT 3
US-09-361-631-2
; Sequence 2, Application US/09361631
; Patent No. 6383778
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Lindemeier, Juergen
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; TITLE OF INVENTION: Involved in Sensory Transduction
; FILE REFERENCE: 02307E-088720US
; CURRENT APPLICATION NUMBER: US/09/361.631
; EARLIER FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: US 60/095.464
; EARLIER FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: US 60/112.747
; EARLIER FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 843
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat G-protein coupled receptor (GPCR) B4 amino
; OTHER INFORMATION: acid sequence
US-09-361-631-1
Query Match 72.7%; Score 3231; DB 3; Length 843;
Best Local Similarity 70.8%; Pred. No. 5.7e-303;
Matches 596; Conservative 109; Mismatches 133; Indels 4; Gaps 2;
QY 1 MGRANKTCSLFFLLWVLAEP---AENSDFVDPDYLGLGFLSLHANNKGVHNLFLQVP 57
DB 1 MGPOARTICLLSLHLVLPKPKLVENSDFHLAGDYLGLGFLSLHANNKGVHNLFLQVP 60
QY 58 MCKEYEVKIVGNLMQAMRFAVEETNNDSLLPGVLLGYEIVDVCYIGNNVQPVLYFLAH 117
DB 61 KNEFTMKVGLNLMQAMRFAVEEINNCSLLPGVLLGYEIVDVCYIGNNVHPLGYFLAQ 120

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RESULT 2
US-09-361-631-1
; Sequence 1, Application US/09361631
; Patent No. 6383778
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Lindemeier, Juergen
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; TITLE OF INVENTION: Involved in Sensory Transduction
; FILE REFERENCE: 02307E-088720US
; CURRENT APPLICATION NUMBER: US/09/361.631
; EARLIER FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: US 60/095.464
; EARLIER FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: US 60/112.747
; EARLIER FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 843
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat G-protein coupled receptor (GPCR) B4 amino
; OTHER INFORMATION: acid sequence
US-09-361-631-1

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241 LLGCDKSTCKRVVYVPMQLLEIWKVNFLLDHOIFPDQGDVALHLEIVQWDRSQNP 300
462 FQSVASYYPLOQLKNTQDLSMHTVNTIPMSMCKRQSGQKQKPVGHVCCFECIDCL 521
301 FQSVASYYPLOQLKNTQDLSMHTVNTIPMSMCKRQSGQKQKPVGHVCCFECIDCL 359
522 PGFLNHTDEYECQACPNNEWSYQSETSCPKQLVFLWEHAPTAVALAALGLFLSTL 581
360 PGFLNHTDEYECQACPNNEWSYQSETSCPKQLVFLWEHAPTAVALAALGLFLSTL 412
582 AILVIFWRHFQPTIVRSAGGPMCFMLTLVLVAVYVVPVYVGPVKYSTCLCRQALFPLCF 641
413 AILVIFWRHFQPTIVRSAGGPMCFMLTLVLVAVYVVPVYVGPVKYSTCLCRQALFPLCF 472
642 TICISCTAVRSFQIVCAFKMASRFPRAYSYVRYQGVYVMAFIVLKMVIVIGMATG 701
473 TICISCTAVRSFQIVCAFKMASRFPRAYSYVRYQGVYVMAFIVLKMVIVIGMATG 532
702 LSPTRTRDPPDKITIVSCNPNRSLNLTSLDILLVSVGFSAVMGKELPTNYNEAKF 761
533 QS-HPRTRDPPDKITIVSCNPNRSLNLTSLDILLVSVGFSAVMGKELPTNYNEAKF 591
762 ITLSMTFYFTSSVSLCTFMSAYSGVLVTIVDILLVNLALSLGFGPKCYMILFYPER 821
592 ITLSMTFYFTSSVSLCTFMSAYSGVLVTIVDILLVNLALSLGFGPKCYMILFYPER 651
822 NTPAYFNSMIQGYTMRD 839
652 NTPAYFNSMIQGYTMRD 669

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; SEQ ID NO 2
; LENGTH: 843
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: mouse G-protein coupled receptor (GPCR) B4 amino
; OTHER INFORMATION: acid sequence
US-09-361-631-2

Query Match
Best Local Similarity 71.6%; Score 3179; DB 3; Length 843;
Matches 582; Conservative 114; Mismatches 142; Indels 4; Gaps 2;

QY 1 MGPRKTIICSLFLLMVLAE---AENSDFYLPDGLGSLFSLHANMKGIHVLNLFQVP 57
Db 1 MGPOARTLHLLFLLHALPKPVMVLGNSDFHLAGDYLGLGFLTHANVKSVSHLSYLQVP 60
QY 58 MCKEYEVKVGYNLMQAMFAVEEINNDSLLPGVLLGYEIVDVVCIYNNVQPVLYFLAH 117
Db 61 KCNEYNMKVLGNLMQAMFAVEEINNCSLLPGVLLGYEMVDVVCYLSNNIQPLGYFLSQ 120
QY 118 EDNLLPIQEDSYNYSRVVAVIPDNSESVMTVANFLSLFLLPQIYSAISDELKDKVRF 177
Db 121 IDDELPLKDYQYRQVAVIPDNSESATVSNLSYFLPQVYSAITDKLQKRRF 180
QY 178 PALLRTTPADHHVAMVQLMLHFRNWIIVLVSSDYGRDNGQLLGERVARR-DICIAF 236
Db 181 PAMLRTPSATHHIEAMVQLMVHFQWNWIVLVSDDDYGRNSHLLSQRLTWTGDIICAF 240
QY 237 QETLPTLPQNMNTSEERQRLVTIVDKLOQSTARVVVVFSPDLTYHFFNEVLNQFTGA 296
Db 241 QVLPVPEPQAVRPEEQDNLNKLKRTSARVVVFSPDLTYHFFNEVLNQFTGA 300
QY 297 VWIASESWAIDPVNLHNLTELHGLTGLTIGTOSVPIPGSEFREWGPQAGPPPLSRTSOS 356
Db 301 VWIASESWAIDPVNLHNLTELHGLTGLTIGTOSVPIPGSEFREWGPQAGPPPLSRTSOS 360
QY 357 YTCNEQCNCLNATISFNTILSGSERVYVSAYVAHALHSLGDCSTKTRVYV 416
Db 361 TTCNODCDACNMTESFNNVLMLSGERVYVSAYVAHALHSLGDCSTKTRVYV 420
QY 417 PMOLLEETKWNFTLLDHOIFDPDQGDVALHIEIVQWQMDRQNPQSVASYPLQRLK 476
Db 421 PMOLLEIWHVNFLLGQLFFDEQDMPMLDIIQWQGLSQNPQSVASYPLQRLK 480
QY 477 NIQDISWHTVNNTPIMSMCKSCQSKQKKPVGIHWCCEICDCLPGTFLNHTEDYECC 536
Db 481 YISNVSWYTPNNTVISMCKSCQSKQKKPVGIHWCCEICDCLPGTFLNHTEDYECC 540
QY 537 ACPNNESYQSTSCFKQLVFLWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIV 596
Db 541 SCPGSMWSYKNNIACFKRLAFLEWHEVPTIVVTLAALGFISTLAILLIFWRHFQTPIV 600
QY 597 RSAGGPMCFMLTLVAVVVPVVGPPKYSTCLCQALFPLCTICISCTAVRSQIV 656
Db 601 RSAGGPMCFMLVPLLLAFGMVVPVVGPPKYSTCLCQALFPLCTICISCTAVRSQIV 660
QY 657 CAFKMASFPFRAYSYYVRVYQGPVSMAPITVLKMWIWMGLATGLSPTRTDPDPKIT 716
Db 661 CVFKMARLPSAYGFWYHGVYVFAITAKVALVAGNMLATTINPIGRTPDDPMII 720
QY 717 IVSCNPNYNSLLFNSTLDLLSVVGFSAFMKELPTNYNEAKFITLSMTFYFTSSVSL 776
Db 721 ILSCHPNYRNGLLFNSTMDLLSVLGFSAFMKELPTNYNEAKFITLSMTFYFTSSVSL 780
QY 777 CTFMSAYSGVLTIVDILVTLNLLAISLGFGPKCYMILFPERTNTPAYNSMTQGYTM 836
Db 781 CTFMSVHDGVLTIMDLLVTLNLLAISLGFGPKCYMILFPERTNTPAYNSMTQGYTM 840
QY 837 RR 838
Db 841 RK 842

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RESULT 4
US-09-134-513-2
; Sequence 2, Application US/09134513
; Patent No. 6210964
; GENERAL INFORMATION:
; APPLICANT: Brown, Edward M.
; APPLICANT: Diaz, Ruben
; APPLICANT: Bai, Mei
; APPLICANT: Quinn, Stephen J.
; TITLE OF INVENTION: The Avian Extracellular Calcium-Sensing
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Vinson & Elkins L.L.P.
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20004-1008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,513
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanzo, Michael A.
; REGISTRATION NUMBER: 36,912
; REFERENCE/DOCKET NUMBER: BR1331/13003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)639-6585
; TELEFAX: (202)639-6604
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1059 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
;
US-09-134-513-2

Query Match
Best Local Similarity 24.6%; Score 1092.5; DB 3; Length 1059;
Matches 284; Conservative 148; Mismatches 354; Indels 105; Gaps 25;

QY 9 CSLPFL--WVLAEPANSDFYLPDGLGSLFSLHANMKGIHVLNLFQVPMCKEYEVKV 66
Db 6 CCLILLFTWNTAYGNQRAQKGDIIILGGLFPIHF--GVAAKD--QDLKSRPESVEC 60
QY 67 IGYNL-----MQAMFAVEEINNDSLLPGVLLGYEIVDVVCIYNNVQPVLYFLA-HED 119
Db 61 IRYNFRGRFWMLOAMFAIEEINNNSPLLNNLPGNLTGRIYFDTCTVSKALEATLSFVAQNKI 120
QY 120 NLLPIQE--DYSNYSRVVAVIPDNSESVMTVANFLSLFLLPQIYSAISDELKDKVRF 177
Db 121 DSLNLDEFNCSEHPISTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSRLLSNKQF 180
QY 178 PALLRTTPADHHVAMVQLMLHFRNWIIVLVSSDYGRDNGQLLGERVARRDICIAFQ 237
Db 181 KSLRTIPNDEHQATAMADIIEYFRNWMVGTIAADDDYGRPIGKFEAREERDIDIFS 240
QY 238 ETLPTLPQNMNTSEERQRLVTIVDKLOQSTARVVVVFSPDLTYHFFNEVLNQFTGAV 297
Db 241 ELI-----SQVSDDEEIQQVVEVI---QNSPARVIVVSSGPDLEPLIKEIVRRNITSKI 292
QY 298 WIASESWAIDPVNLHNLTELHGLTGLTIGTOSVPIPGSEFREWGPQAGPPPLSRTSOS 357
Db 293 WLASEWASSSLIAMPEFFRVRIGTIGFALKAGQIPGFREFLQ---KVHPKKSANNGFAK 349

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QY 358 TCNQCNDCL-----NATLSFN----- 374
 Db 350 EFWEETFNCLPSEKNSPASAFKHAERGLAGNGTAAPRPTCDENITSVETPYMD 409
 QY 375 -TILRLSGERVVSVYSAVAVAHALHSLGCG-----DKSTCKRVVVPWOLLIEIW 425
 Db 410 FTHLRIS-----YNYLAVYSIAHALQDIYTCIPKGLFNGSCADIKKVEAMQVLKHLR 464
 QY 426 KVNFTL-LDHQIFPDQGDVALHLEIVQWMDRSQNP--FQSVASYPL-----ORQLKNI 478
 Db 465 HLANFTSNWGEQVDFDEFGDLGVNYSIINWHLSPEDSGVFEVGHYNYAKKGRRLPINE 524
 QY 479 QDISWHTVNNITPMSMCKRCQSQOKKPV-GIHVCCFECIDCLPGTFLNHTEDYEYCOA 537
 Db 525 NKILWSGFSKEVPFNSCRDCLPGRKGIIEGTEPCCFECVDCPDGBYSDET-DASACDK 583
 QY 538 CPNNEWSYQSETSCFKQLVFEWHEAPTIALLAALGFLSTLAILVFWHRHPTPIVR 597
 Db 584 CPEDYWNENHTSCIPKQIBFLSWTEPPGIALTLFAVLGIFLTGFLVGVFTKFRNTPIVK 643
 QY 598 SAGGPMCFMLTLTLVAYMVVVPVGGPKVSTCLCROALPPLCTICICIAVRSFQIVC 657
 Db 644 ATNRELSYLLLFSLCCFSSLLFTIGEPQNWTCRLROPAGFISFVLCTICILVKTNRVLL 703
 QY 658 AFKMASREPPRA-YSYVWRYQGPVYSMAFITVLMVIVVIGMLATGLSPTTRTDPPDKIT 716
 Db 704 VFE--AKIPTSLHRKMWGLNLOFLLVFLCTFPQIVICVI-WLYTAPSSYRNHELEDEII 760
 QY 717 IVSCNPNYRNLSLNTSLLDLSLVVGFSAFYMKGKELPTNYNEAKFITLSMTFYFTSSVSL 776
 Db 761 FITCHESLMALGFLIGYTCLLAALCFFAFKSKRLPENFNEAKFITFSMLIFFIVMIS- 819
 QY 777 CTFMSAYSGVLVITVDLLVTVNLNLALSGLG----YFGPKCYMILFYPERNT 823
 Db 820 --FIPAYASTYKGFVS-AVEVIALAASFGLLACIFFNKNVYIILFKPSRNT 867
 RESULT 5
 US-09-162-021B-2
 ; Sequence 2, Application US/09162021B
 ; Patent No. 6337391
 ; GENERAL INFORMATION:
 ; APPLICANT: H. William Harris
 ; APPLICANT: Edward M. Brown
 ; APPLICANT: Steven C. Hebert
 ; TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic
 ; FILE REFERENCE: 2856.1001-007
 ; CURRENT APPLICATION NUMBER: US/09162,021B
 ; CURRENT FILING DATE: 1998-09-28
 ; PRIOR APPLICATION NUMBER: PCT/US97/05031
 ; PRIOR FILING DATE: 1997-03-27
 ; PRIOR APPLICATION NUMBER: 08/622,738
 ; PRIOR FILING DATE: 1996-03-27
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 1027
 ; TYPE: PRT
 ; ORGANISM: Squalus acanthias
 US-09-162-021B-2
 Query Match 24.5%; Score 1089; DB 3; Length 1027;
 Best Local Similarity 31.1%; Pred. No. 1e-95;
 Matches 278; Conservative 161; Mismatches 360; Indels 96; Gaps 26;
 QY 5 AKTICSLPFLMVLAPPAENSDFYLP-----GDVLLGGLFSLHANM--KGIVHLNFIQ 55
 Db 2 AQHCOLLEFLGFTLLO-SYNSVSGYGNQRAQKGGDIILGGLFPIHFGVAAQODLKSREPE 60
 QY 56 VPMCKEYEVKVIYGNLQMAMRFAVEBINNDSLLPGVLGYIVDVC-YISNNVQPVLYF 114

Db 61 ATKCIYRNER--GFRWLQAMIFAIBEINNSMTFLPNITLGYRIPTDTCNTVSKALEATLSF 118
 QY 115 LA-HEONLLPIQEB--DYSNYSIRVAVIGPNDSESVMVAVANFLSLFLLPQITYSASIDEL 171
 Db 119 VAQNKISLMDLDFCNSDHIPTSTIAVVGATGGISTAVANLLGLFIPQVSYASSRLL 178
 QY 172 RDKVRFPALLRTTPSADHVEAMVQMLMFRWNIIIVLVSSDYYGRONGQLLGRVARRD 231
 Db 179 SNKNEYKALRTIPNDEQQATAMAEIIIEHPQWVWVGTAAADDDYGRGIDKDFREEAVKRD 238
 QY 232 ICIAFOBTTLPTLPQNMNTSEERQRLVTVIDKLOOSTARVVVPSPLTILYHPFNEVLRL 291
 Db 239 ICIDFSEMI-----SQYIT---OKLEFIADVIQNSSAKVVIVFNSGPDLEPLIQEIYVR 290
 QY 292 NFGTCAVWIASWALDPVLNHLTELGLHGLTFLGIIQSVPIPGFSEPRE----- 340
 Db 291 NITDRIWIASWASSSLIAKPEYFHVVGTTIGFALRAGRIPGNKELKEVHPSSSDNG 350
 QY 341 -----W-----GPOA-GPPPLSRTSQSVTCNQECNCLNAT 370
 Db 351 FVKEFWBETFCYFTEKTLTQLKNSKVPESHGPAAGDGSKAGNSRRRTALRHPCTGSENI 410
 QY 371 LSEFTILRLSGERVVSVYSAVAVAHALHSLGCKST-----CTK-RVYVWPOLLE 422
 Db 411 SVETPYLDYTHLRISYNYVAVYSIAHALQDIHSCKEGTGIFANGSCADIKKVEAMQVLN 470
 QY 423 EIKVNTT-LLDHQIFPDQGDVALHLEIVQWMDRSQNP--FQSVASY-----YPLORQL 475
 Db 471 HLLHLKFTNSMGEQVDFDQDGLKGNVTIINWQLSAEDESVLFPHEVGNVAYAKPSDRLN 530
 QY 476 KNIQDISWHTVNNITPMSMCKRCQSQOKKPV-GIHVCCFECIDCLPGTFLNHTEDYE 534
 Db 531 INEKKILWSGFSKVPVFNCSRDVCPGTRKGIIEGTEPCCFECMACAEGEP-SDENDASA 589
 QY 535 COACPNEWSYQSETSCFKQLVFEWHEAPTIALLAALGFLSTLAILVFWHRHPTP 594
 Db 590 CTKPNDFWNSNHTSCIAKEIYLSWTEPPGIALTLFAVLGILITISFVLGVFIKFRNTP 649
 QY 595 IVRSAGGPMCFMLTLTLVAYMVVVPVGGPKVSTCLCROALPPLCTICICIAVRSFQ 654
 Db 650 IVKATNRELSYLLLFSLICCFSSSLIFIGEPRDWTCLRLQOPAFGISFVLCISLIVKTNR 709
 QY 655 IVCAFKMASREPPRA-YSYVWRYQGPVYSMAFITVLMVIVVIGMLATGLSPTTRTDPPD 713
 Db 710 VLLVFE--AKIPTSLHRKMWGLNLQFL-LVFLCILVQIVTCIIMLYTAPSSSYRNHELED 766
 QY 714 KITIVSCNPNYRNLSLNTSLLDLSLVVGFSAFYMKGKELPTNYNEAKFITLSMTFYFTSS 773
 Db 767 EVIFITDEGSLMALGFLIGYTCLLAALCFFAFKSKRLPENFNEAKFITFSMLIFFIVW 826
 QY 774 VS-LCTFMSAYSGVLVITVDLLVTVNLNLALSGLYFG----PKCYMILFYPERNT 823
 Db 827 ISFIPAYVSTY-GKRVSAVE----VIALASSFGLGCIYFNKCVIILFKPCRN 876
 RESULT 6
 US-10-268-051-8
 ; Sequence 8, Application US/10268051
 ; Patent No. 6748900
 ; GENERAL INFORMATION:
 ; APPLICANT: Harris, H. William
 ; APPLICANT: Jury, Steven
 ; APPLICANT: Russell, David R.
 ; APPLICANT: Nearing, Jacqueline A
 ; APPLICANT: Betka, Marlies
 ; APPLICANT: Linley, Timothy
 ; APPLICANT: Brown, Edward M
 ; TITLE OF INVENTION: Methods for Growing and Imprinting Fish Using an Odorant
 ; FILE REFERENCE: 2213.2004-001
 ; CURRENT APPLICATION NUMBER: US/10/268,051
 ; CURRENT FILING DATE: 2003-01-24
 ; PRIOR APPLICATION NUMBER: 60/328,464
 ; PRIOR FILING DATE: 2001-10-11

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; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1027
; TYPE: PRT
; ORGANISM: Squalus acanthias
US-10-268-051-8

Query Match          24.5%; Score 1089; DB 4; Length 1027;
Best Local Similarity 31.1%; Pred. No. 1e-95;
Matches 278; Conservative 161; Mismatches 360; Indels 96; Gaps 26;

QY 5 AKTICSLFLLWLAEPANSDPYLP-----GDYLLGGLFSLHAM--KGIVHLNFIQ 55
Db 2 AQLHCQLLFLGFTLLQ-SYVSGYGNQRAKKGDIIILGLFPIHFGVAAQDLSRPE 60
QY 56 VPMCKEYEVKIVGYNLMQAMRFAVEINDDSLPGVLLGYEIVDVC-YISNNVQPVLYF 114
Db 61 ATKCIRYNFR--GFRWLQAMIFAIEINNSMTFLFNITLGYRIFDTCNTVSKALEATLSF 118
QY 115 LA-HEDNLLPIQE--DYSNYISRVAVIGPDNSESVMTVANFLSLFLLPQITYAISDEL 171
Db 119 VAQNKIDSLNLDPCNSDHIPTIAVVGATSGISTAVANLLGLFYIPQVSIASSRLL 178
QY 172 RDKVRFPALLRTPSADHHVAMVLMHFRWNWIIIVSSDPTGRDNGQLLGERVARD 231
Db 179 SNKNEYKAFLRTPNDEQOATAMABIIIEHFQWNVGTTLAADDYGRPGIDKPREBAVKGD 238
QY 232 ICIAFOETLPTLOPNQNTSEBQRLVITVDKLOQSTARVVVFPDLYLHYFFNEVLQ 291
Db 239 ICIDFSEMI-----SQYVT--OKOLEFTADVIQNSAKVIVVFSNGPDLPLIOEIVRR 290
QY 292 NFGAVIASBSWALDPVHLNLTGLHGTITQSVPIPGSEFRE-----340
Db 291 NITDRIWLASEAWSSSLIAKPEYHVVGTTGFPALRAGRIPFNKFLKEVHPSSSDNG 350
QY 341 -----W-----GPOA-GPPPLSRTSQSYTCNQCDNCLNAT 370
Db 351 FVKEPWEETFCYFTEKTLTQKNSKVPESHGPAQGDGSKAGNSRRTALRHPTCEENIT 410
QY 371 LSFNTILRSGERVYVYSAVAVAHLSLLGCDKST-----CTK-RVVPWQELLE 422
Db 411 SVETPYLDYTLRISYVYVAVYSAHALQDTHSCKPGTGIFANGSCADIKKVEAWQLN 470
QY 423 BIWKVNF--LLDHOIFFPDQGVVALHLEIVOWDQRSONP--FQSVASY-----YPLQRL 475
Db 471 HLLHLKFTNSGEQVDFDDQGLKGNYYIINQLSAEDSVLFHEVGNVNAVAKPSDRIN 530
QY 476 KNIODISWHTNNTIPMSCKRQSGQKKPV-GIHVCCFECIDCLPGTFLNHTDEBYE 534
Db 531 INEKKILMSGFSKVVPFNSCRDVPGRKGIIEGEPTCCFECMACABGEF--SDENDASA 589
QY 535 COACPNEMWSQSETSCFKRQIVLEWHEATIAVALLAAGFLSTAILVIFWPHFOTP 594
Db 590 CTKCPNDPWSNENHTSIAKEIYLSWTEPFGIALTIIFAVILGILTSFVLGVFKFRNTP 649
QY 595 IVRAGGPMCLMLTLILLVAVYVVPVPPKVKSTCLCRQALFPLCFTICISCIASVRSQ 654
Db 650 IVKATNRLSYLLLFSLICCCSSSLIFIGERPDWTCRLRQAPAGISFVICISCLVKTR 709
QY 655 IVCAFPMASRFPRA-YSVWRYQGVVSMATITVLKMWIVVIGMATGLSPTRTDDPD 713
Db 710 VLLVPE--AKIPTSLHRKWVGLNLQFL-LVFLCILVQIVTCIIWLYTAPPSSYRNHELED 766
QY 714 KITIVSCNPNVNSLLFNSTLDLLSVVGVFSFAYMGKELPTNYNEAKTITISMTFYTSS 773
Db 767 EVIFITCDGSLMGLFGLIGYTCLLAAICFFFAFKSKLPENFNEAKEITFSMLIFFTW 826
QY 774 VS-LCTFMSAYSGLVITVDLLVTLVNLALISLGVFG-----PKCMWILFYPERNT 823
Db 827 ISFIPAYVSTY-GKFSVAVE-----VIALASSFGLLGCIVFNKCYIILFKPCRNT 876

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RESULT 7
US-08-485-588-7
; Sequence 7, Application US/08485588
; Patent No. 568938
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: Forrest H. Fuller
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485.588
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 483-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1078 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-588-7

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Query Match          24.3%; Score 1079.5; DB 1; Length 1078;
Best Local Similarity 31.4%; Pred. No. 9.1e-95;
Matches 279; Conservative 160; Mismatches 342; Indels 107; Gaps 27;

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QY 16 WVLAEPAENSDPYLP-----GDYLLGGLFSLHAMKGIVHLNFIQVPMCKEYEVKIVG 68

Db 8 WLLALTWHTSAYCPDQRAQKGDIIIGGLFPIHF---GVAARD--QDLKSRPESVEICR 62
QY 69 YNL-----MOAMFAVEEINNDSSLLPGVLLGYEIVDVC-YISNNVQPVLYFLA-HEDNL 121
Db 63 YNFRGFWLOAMIFAIBEINSSPALLNLTIGRIPDTCTNTVSKALEATLSFVAQNKIDS 122
QY 122 LPIQE--DYSNVI SRVAVIGPNSESVMTVANFLSLFLLPQITYSAISDELDRKVRPPA 179
Db 123 LNLDEFNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSASSRLLSNKNQFS 182
QY 180 LLRTTSPADHHVAMQVLMHFRWNWIIIVSSDTYGRDNGQLLGERVARDICIAFOET 239
Db 183 FLRTIPNDEHQATAMADIIIEYFRWNWVGTIAADDDYGRPGIEKPREAEERDICI DFSEL 242
QY 240 LPTLPQNMNTSEERQRLVITVDKLOQSTARVVVVRSPDLTLHYHFFNEVLNRQFTGAVMI 299
Db 243 I-----SQYDEEIQHVVEVI---QNSTAKIIVFSSGPDLEPLIKEIVRNTITGKIWL 294
QY 300 ASWSAIDPVLHNLTELHGLTFTGLITIQSVPIPGFSEF-----REWGPO 344
Db 295 ASEAWASSLLIAMPQYFHVVGTTIGFALKAGQIPGREFLLKVKHPRKSVHNGPAKEFWE 354
QY 345 A-----GPPPLSRTSOTYCNQECNCLNATLSFNTILRSGE----- 382
Db 355 TFNCHLOEGAKGPLVDFTLRGH--EESGRFNSSTAFRPL--CTGDENISSVETPYID 410
QY 383 ----RVVYSVYSAVAHAHLSLGC-----DKSTCKRVVYPWQLLEEIKWYNFT 430
Db 411 YTHURISYVLAIVSTAHALQDIYTCPLGRGLTNGSCADIKKVEAWVLKHLRHLNFT 470
QY 431 -LLDHQIFFDPQGDVALHLEIVQWDRSQNP--FQSVASYPL-----ORQLKNIQDIS 482
Db 471 NNMGEQVTFDCGLDVGNSIINWHLSPEDGSIIVFKEV-GYNNVYAKKGERLFTNEEKIL 529
QY 483 WHTVNTIPMSKRCOSGQKKPV-GIHVCCPECIDCLPGTFLNHTEDYEQACPNV 541
Db 530 WSGFSREVFPNCSRDCLAGTRKGIIEGTECCFECVCPDGEYSDET-DASACNKCDD 588
QY 542 EWSQSETSCFKQVLVLEHAEPTIAVALLAALGFLSTLAILVFNHFTPTIVRSAGG 601
Db 589 FWSNHTSCIAKEIFUSWTEPGIALTLFAVIGIFLTAFLVGVFKFRNTPIVKATNR 648
QY 602 PMCFMLTLVLVAVVVPVYVGPVKVSTCLCRQALFPLCFTICISIAVRSFQIVCAP-- 659
Db 649 ELSVLLFSLCCPSSUFFIGEPODWTCLRQPAFGISFVLCISCLVKNRVLNVEA 708
QY 660 KMAFRFPAYSWRYQPYVSMFAITVLKMWIVVIGMLATCLSPTRTDPDPKTIIVS 719
Db 709 KIPTSFRKQ--WNGLNLFLLVFLCTFMQIVCVI-WLYTAPSSYRNQBLEDEIIFIT 764
QY 720 CNPNYRNLLENTSLLDLSVVGFSAVMGKELPTNYNEAKFITLSMTFYFTSSVSLCTF 779
Db 765 CHEGSLMALGFLIGYTCLLAICFFAFKSRKLPENFNEAKFITFSMLIFIVWIS---F 821
QY 780 MSAYSGVLVITVDLVTVNLNLAISLG----YFGPKCYMILFYPERNT 823
Db 822 IPAYASTYKGFVS-AVEVIAIILAAFGLLACIFENKIYIILFKPSRNT 868

RESULT 8

US-08-484-565-7

; Sequence 7, Application US/08484565

; Patent No. 5763569

; GENERAL INFORMATION:

; APPLICANT: Edward M. Brown

; APPLICANT: Steven C. Hebert

; APPLICANT: James E. Garrett, Jr.

; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE

; TITLE OF INVENTION: MOLECULES

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: First Interstate World Center

STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,565
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-565-7

Query Match 24.3%; Score 1079.5; DB 1; Length 1078;

Best Local Similarity 31.4%; Pred. No. 9.1e-95;

Matches 279; Conservative 160; Mismatches 342; Indels 107; Gaps 27;

QY 16 WVLAEPAENSDFYLP-----GDYLLGGLPSLHANKMGI VHLNPLQVPMCKEYEVKVG 68
Db 8 WLLALTWHTSAYCPDQRAQKGDIIIGGLFPIHF---GVAARD--QDLKSRPESVEICR 62
QY 69 YNL-----MOAMFAVEEINNDSSLLPGVLLGYEIVDVC-YISNNVQPVLYFLA-HEDNL 121
Db 63 YNFRGFWLOAMIFAIBEINSSPALLNLTIGRIPDTCTNTVSKALEATLSFVAQNKIDS 122
QY 122 LPIQE--DYSNVI SRVAVIGPNSESVMTVANFLSLFLLPQITYSAISDELDRKVRPPA 179
Db 123 LNLDEFNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSASSRLLSNKNQFS 182
QY 180 LLRTTSPADHHVAMQVLMHFRWNWIIIVSSDTYGRDNGQLLGERVARDICIAFOET 239
Db 183 FLRTIPNDEHQATAMADIIIEYFRWNWVGTIAADDDYGRPGIEKPREAEERDICI DFSEL 242
QY 240 LPTLPQNMNTSEERQRLVITVDKLOQSTARVVVVRSPDLTLHYHFFNEVLNRQFTGAVMI 299

Db 243 I-----SQYDEEIQHVVEVI---QNSTAKVIVVFSSGPDLEPLKEIVRNRITGKIWL 294
QY 300 ASESALDVLNHLTELGHGFLGTTIGSVIPGSEF-----REWGPO 344
Db 295 ASEAWASSLIAMPQYFHVVGTTIGFALKAGQIPGREFLKKVHPKSVHNGFAKEFEE 354
QY 345 A-----GPPPLSRTSQSYTCNQECNCLNATLSFNTILRLSGE----- 382
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QY 383 ----RVVSVISAVYAVAHALHSLGC-----DKSTCTKRVVYPQOLLEIKWKNFT 430
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Db 530 WSGFSEVPFNSCRDLGATKGIIEGPTCCPECVECPGEYSDET-DASACNKCDD 588
QY 542 EWSQSETSCPKQVLVFLWEHAPTIAVALLAAGFLSTLAILVIFWRHFQTPVRSAGG 601
Db 589 FWSNENHTSCIAKETIEFLSWTEPPFGIALTLFAVLGIFLTAFLVGFIFKRNTPIVKATNR 648
QY 602 PMCFMLLTLVAVMVVPPVPPKVSCLCRQALFPLCFTICISCIARSFQIVCAF-- 659
Db 649 ELSYLLLESLLCCSSSUFFGEPQDWTCLRQAPAFISFVLICISILVKNRVLVFEA 708
QY 660 KMASRFPRAYSYVRYQGYVSMFIVLKMVIVVIGMLATGLSPTRTDPDPKITIVS 719
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QY 720 CNPNYRNLNTSLDILLVVGVSFAYMGKELPTNYNEAKPITLSMTFTYTSVSLCTP 779
Db 765 CHEGSMALGLIGYTCLLAIAICFPFAFKSKLPENFEAKPITPSMLIFFIVWIS--F 821
QY 780 MSAYSGVLVTVDLVTNLNLAISLG---YFGPKCYMILPYPERNT 823
Db 822 IPAYASTYKGFVS-AVEVIALAASFGLLACIFFNKIYIILLFKPSRNT 868
RESULT 9
US-08-480-751-7
; Sequence 7, Application US/08480751
; Patent No. 5858484
; GENERAL INFORMATION:
; APPLICANT: Edward F. Nemeth
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: Forrest H. Fuller
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,751

; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1078 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-480-751-7

Query Match 24.3%; Score 1079.5; DB 2; Length 1078;
Best Local Similarity 31.4%; Pred. No. 9.1e-95;
Matches 279; Conservative 160; Mismatches 342; Indels 107; Gaps 27;

QY 16 WLAEPAENSDFYLP-----GYLLGLGFLSLANMKGIHVLNPLQVPMCKEYEVKVG 68
Db 8 WLLALTWHTSAYGPDQPAQKKGDIIIGLGLPIHF---GVAKD--QDLKSRPESVECI 62
QY 69 YNL-----MQAMRFAYEEINNDSSLLPGVLGLGYBIVDVC-YISNNVQPVLYFLA-HEDNL 121
Db 63 YNFRGRWLQAMIFAIBEINSSPALLPNLTGLGYRIFDTCNTVSKALEATLSFVAQNKIDS 122
QY 122 LPIQ--DYSNYSIRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELKVRPPA 179
Db 123 LNLDFECNSHESHPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSRLLSNKQPKS 182
QY 180 LLRTTPSADHHEAMVOLMLHFRWNVIIVLVSSDYGRDNGQLLGERVARDICIAQET 239
Db 183 FLRTIPNDEHOATAMADIIYFRWNVWGTAAADDYGRPGIEKPREAEERDICI DISEL 242
QY 240 LPTLQPNQNTSEERQRLVTIVDKLOQSTARVVVVFSPDLTYHFFNEVLRQNTGAWVI 299
Db 243 I-----SQYDEEIQHVVEVI---QNSTAKVIVVFSSGPDLEPLKEIVRNRITGKIWL 294
QY 300 ASESALDVLNHLTELGHGFLGTTIGSVIPGSEF-----REWGPO 344
Db 295 ASEAWASSLIAMPQYFHVVGTTIGFALKAGQIPGREFLKKVHPKSVHNGFAKEFEE 354
QY 345 A-----GPPPLSRTSQSYTCNQECNCLNATLSFNTILRLSGE----- 382
Db 355 TFNCHLOEGAKGFLPVDFTFLRGH--EESGDRFSNSTAFRPL--CTGDENISSVETPYID 410
QY 383 ----RVVSVISAVYAVAHALHSLGC-----DKSTCTKRVVYPQOLLEIKWKNFT 430

Db 411 YTHLRISYNYLAVYSIAHALQDIYTCPLGRGLFTNGSCADIKKVEAWQVLKHLRLHNT 470
Qy 431 -LLDHOIFDPQGDVALHLEIVQWDRSNP--FQSVASYPL-----ORQLNKIDIS 482
Db 471 NNMGEQVTFDECDGLVGNYSIINWHLSPEDGSIVFKEV-GYNNYAKKGERLFINEEKIL 529
Qy 483 WHTVNNTIPMSMCKSCQSQKKPV-GIHVCCFECIDCLPGTFLNHTDEYEQACPNN 541
Db 530 WSGFSREVPSNCRDLCTAGTRKGIIEGPTCCFCEVCECPDGEYSDT-DASACNKPDD 588
Qy 542 EWSYQSETSCFKQLVPLEWHEAPTTIAVALAALGFLSTAILVIFWRHQTPIVRSAGG 601
Db 589 FWSNENHTSCIAKEIEFLSWTEPGIALTLFVGLGFLTAFLVGLFKERTPIVKATNR 648
Qy 602 PMCFMLTLLVAVMVVVPVGVKYSTCLCRQALPCLCTICISCIATVRSFOIVCAF-- 659
Db 649 ELSYLLFLSLLCCFSSLLFFIGFPQDWTCKLRQAFGISVLCISCLLVKINRVLVFEA 708
Qy 660 KMASRFPFRAYSVMRYQGPVSMAPITVLKXVIVVIGMLATGLSPTRTDDPKITIVS 719
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Qy 720 CNWYRNSLLPNTSLDLLSVGFSFAYMKGELPTNNNEAKPITLSMTFFYFTSVSLCTF 779
Db 765 CREGSLMALGFLICYTCLLAAICFFFAFKRKLPENFENAKFITFSLFIIVMIS---F 821
Qy 780 MSAYSGVLTIVDVLVTLNLLAISLG---YFGPKCYMILFPERNT 823
Db 822 IPAYASTYGRFVS-AVEVIALAASFGLLACIPFNKIYIILFKPSRNT 868

RESULT 10
US-08-943-986-7
; Sequence 7, Application US/08943986
; Patent No. 5962314
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,986
; FILING DATE: 03-OCT-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,565
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993

; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1078 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-943-986-7

Query Match 24.3%; Score 1079.5; DB 2; Length 1078;
Best Local Similarity 31.4%; Pred. No. 9.1e-95;
Matches 279; Conservative 160; Mismatches 342; Indels 107; Gaps 27;

Qy 16 WVLAEPAENSDFYLP-----GDYLLGLFSLHANMKGIVHLNFIQVPMCKEYEVKVG 68
Db 8 WVLALTWHTSAYGPQRAOKGDIILGGLFPIHF---GVAARD---QDLKSRPESVEICR 62
Qy 69 YNL-----MQAMRFVAVEEINNDSLLPGVLLGYEIVDVC-YISNNVQPVLYFLA-HBDNL 121
Db 63 YNFRGFRWLQAMIFATEEINSSPALLPNLTGRIPTDCTNTVSKALEATLSFVAQNKIDS 122
Qy 122 LPLOE-DYSNYLSRVVAVIGPNSSVMVAVNLSFLPLQITYSALSDELDRKVFPA 179
Db 123 LNLDEFNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSSSLLSKNNOFKS 182
Qy 180 LKRTTSPADHHVAMVQLMLHFRWNITVLVSDTYGRDNGQLLGERVARRDICIAFOET 239
Db 183 FLRTIENDEHQATAMADIIYFRWNVGTIAADDDYGRPGIEKFEREAERDIDISEL 242
Qy 240 LPTLPQNQNTSBERQLVTIVDKLOQSTARVVVWFSPDLTLXHPFNEVLQNFTGAWMI 299
Db 243 I-----SQSDEBEIQHVEVI---QNSTAKVIVWFSSGPDLEPLIKEIVRRNITGKIWL 294
Qy 300 ASSSWAIDPVHLNLTGLHGTPLGITIQSVPIPGFSEF-----REWGPO 344
Db 295 ASEAWASSLIAMPQYFHVVGTTIGFALKAGQIPGFREFLKKVHPKRSVHNGFAKEPWE 354
Qy 345 A-----GPPLSRTSQSYTCNQCNCNCLNATLSFNTILRLSGE----- 382
Db 355 TFNCHLOEGAKGPLVDVTFIRGH--ESGDRFNSSTAFRPL--CTGDEMISSETPYID 410
Qy 383 ----RVVYSVYSVAVYVAHALHSLGC-----DKSTCTKRVVYVWQVLEETKWNFT 430
Db 411 YTHLRISYNYLAVYSIAHALQDIYTCPLGRGLFTNGSCADIKKVEAWQVLKHLRLHNT 470
Qy 431 -LLDHOIFDPQGDVALHLEIVQWDRSNP--FQSVASYPL-----ORQLNKIDIS 482
Db 471 NNMGEQVTFDECDGLVGNYSIINWHLSPEDGSIVFKEV-GYNNYAKKGERLFINEEKIL 529
Qy 483 WHTVNNTIPMSMCKSCQSQKKPV-GIHVCCFECIDCLPGTFLNHTDEYEQACPNN 541
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Qy 542 EWSYQSETSCFKQLVPLEWHEAPTTIAVALAALGFLSTAILVIFWRHQTPIVRSAGG 601
Db 589 FWSNENHTSCIAKEIEFLSWTEPGIALTLFVGLGFLTAFLVGLFKERTPIVKATNR 648
Qy 602 PMCFMLTLLVAVMVVVPVGVKYSTCLCRQALPCLCTICISCIATVRSFOIVCAF-- 659

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709 KIPTSFRK---WMLNLQFLVFLCTFMQIVCVI-WLYTAPPSYRQOELEDEIIFT 764 Db
720 CNPNYRNSLLFNTSLDILLSVVUGSEAYMGKELPTVYNEAKFTLSLWTFVSSVSLCTF 779 QY
765 CHEGSLMALGELIGYTCLLAAICFFPAFKRKLPEFNFAKFTFSLMFIIFWIS---F 821 Db
780 MSAYSGVLITVDLTVTLNLALSLG----YFGPKCYMILFYPERNT 823 QY
822 IPAYASTYKGKFS-AVEYIALAASFGLLACIFENKIYIILFKPSRNT 868 Db

RESULT 11

US-08-353-784-7
Sequence 7, Application US/08353784
Patent No. 6011068
GENERAL INFORMATION:
APPLICANT: Edward F. Nemeth, Edward M.
APPLICANT: Brown, Steven C. Van Wagonen, Manuel
APPLICANT: Bradford C. Van Wagonen, Manuel
APPLICANT: F. Balandrin, Forrest H. Fuller,
APPLICANT: Eric G. DelMar, and Scott T. Moe
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,784
FILING DATE: 9 December, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 8
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 209/069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

Query Match 24.3%; Score 1079.5; DB 3; Length 1078;
Best Local Similarity 31.4%; Pred. No. 9.1e-95;
Matches 279; Conservative 160; Mismatches 342; Indels 107; Gaps 27;


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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,588
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-588-8

Query Match 24.2%; Score 1075; DB 1; Length 1079;
Best Local Similarity 31.4%; Pred. No. 2.5e-94;
Matches 282; Conservative 166; Mismatches 327; Indels 124; Gaps 33;

QY 10 SLFLLVLAEPRENSDFYLP-----GDYLLGLFSLHNMKGIVHNLFLQVPMCKEY 62
DB 9 ALLALAW-----HSSAYGPDQRAQKKGDIILGLFPIHF--GVAAKD--QDLKSRPE 56
QY 63 EVKVIQYNL-----MQAMRAVEEINNDSSLLPGVLLGYEIVDVC-YISNNVQVLYFLA 116
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QY 117 -HEDNLLPIQE--DYSNYSIRVAVIGPDNSVMTVANFLSLFLLPQITYSALSDELRD 173
DB 117 QNKIDSLNDEFNCSEHPSHTIAVVGATGSGVSTAVANLLGLFYIPQVSASSRLLSN 176
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DB 177 KNOYKSPRTIPNDEHOATWAOIEFYRWNVGTIAADDDYGRPGTEKFEAEERDIC 236
QY 234 IAFQETLPTLPQNMNTSEERQRLVTIVDKLQOSTARVVVFSPLDLYHFFNEVLQNF 293
DB 237 IDFSLEI-----SQYSEEBEIQVVEVI---QNSTAKVIVVFSGPDLEPLIKEIVRNI 288
QY 294 TGAVWIASGWAIDPVLNHTLGLH-LGTFIGITIQSVPIPGSEF----- 338
DB 289 TGRWLASAWASSSLI-AMPEYFHVVGTTGIFGLKAGQIPGGRFELQVHKPRXSVHNGF 347
QY 339 -REWGPOA-----GPPPLSRTSQSYTCNCECNCLNATLSENTILRLSGE----- 382
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RESULT 15

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US-08-484-565-8
; Sequence 8, Application US/08484565
; Patent No. 5763569
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,565
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993

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424 IMKVNET-LLDHQIFPDPOGDVALHLEIVQWDRSQNP--FOSVASIYPL-----QRQL 475
464 LRHLNFTNMGEQVTFDECQDLVGNYSIINWHLSPEDGSIVFKEV-GYNNVYAKGERLF 522
476 KNIQDISWHTVNTIIPMSCKRCSQSGOKKPV-GIHVCCFECIDCLPGTFLNHTDEYE 534
523 INEEKILMSGFREVFPVSCSDCQAGTRKGIIEGPTCCFCEVCEPDGEYSGET-DASA 581
535 CQACPNNEWSYQSETSCFKRQLVFLWEHEAPTTIAVALLAALGFLSTLAILVIFWRHPQTP 594
582 CDKCPDDFWSNENHTSCIAKEIEFLAWTEPFGIALTLFAVLGIFLTAFLVGLVEIKFRNTP 641
595 IYRSAGGPMCFMLTLLVYAVVYVYVGGPKVKSTCLCQALPFLCFTICISIAVRSFQ 654
642 IVKATNRELSYLLFLSLLCCFSSSFFIGEPQDTRLRQPAFGISFVLCSICILVKTNR 701
655 IVCAFKWASGRPRAY--SYM-VRYQGPVYSMAFITVLKMWIVVIGMLATGLSPTRTDPD 711
702 VLLVFB--AKIPTSFRKWKWGLNLQ---FLVFLCTFMQILLICIIWLYTAPPSYRNHEL 756
712 DPKITIVSCNPNYRNSLLFNTSL---DLLSVVVGFSFAYMGKELPTNNEAKTITUSMTF 768
757 EDEIIFITC---HEGSLMALGSLIGVTCLLAAICFPFAFKSRKLPENFNEAKTITFSMLI 813
769 YFTSSVSLCTFMSAYSGVLVTIVDILLVTLNLAISLG-----YFGPKCYMILFPENPT 823
814 FFIWIS--FIPAYASTYGKFVS-AVEVIAILAA3FGLLACIFFNKNVYIILPKPSRNT 868

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 30, 2004, 13:54:59 ; Search time 150 Seconds
(without alignments)
1983.926 Million cell updates/sec

Title: US-10-035-045-21

Perfect score: 4443

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1575965 seqs, 354694765 residues

Total number of hits satisfying chosen parameters: 1575965

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
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21: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4443	100.0	839	14	US-10-035-045-21
3	4443	100.0	839	14	US-10-179-373-6
4	4443	100.0	839	16	US-10-725-103-6
5	4443	100.0	839	16	US-10-725-489-6
6	4443	100.0	839	16	US-10-725-080A-6
7	4443	100.0	839	17	US-10-725-472A-6
8	4443	100.0	839	17	US-10-725-276-21
9	4443	100.0	839	17	US-10-770-127-198
10	4422	99.5	839	14	US-10-246-785-4
11	4392.5	98.9	838	10	US-09-927-315-9
12	4392.5	98.9	838	14	US-10-190-417-9
13	3463.5	78.0	669	13	US-10-124-598-7

14	3463.5	78.0	669	14	US-10-096-144-7	Sequence 7, Appli
15	3463.5	78.0	669	14	US-10-225-567A-683	Sequence 683, App
16	3231	72.7	843	10	US-03-927-315-7	Sequence 7, Appli
17	3231	72.7	843	13	US-10-124-598-1	Sequence 1, Appli
18	3231	72.7	843	14	US-10-096-144-1	Sequence 1, Appli
19	3231	72.7	843	14	US-10-246-785-6	Sequence 6, Appli
20	3231	72.7	843	14	US-10-190-417-7	Sequence 7, Appli
21	3231	72.7	843	14	US-10-179-373-17	Sequence 17, Appli
22	3231	72.7	843	15	US-10-436-715-38	Sequence 38, Appli
23	3231	72.7	843	15	US-10-436-715-70	Sequence 70, Appli
24	3231	72.7	843	16	US-10-725-103-17	Sequence 17, Appli
25	3231	72.7	843	16	US-10-725-489-17	Sequence 17, Appli
26	3231	72.7	843	16	US-10-725-080A-17	Sequence 17, Appli
27	3231	72.7	843	17	US-10-725-472A-17	Sequence 17, Appli
28	3179	71.6	843	10	US-03-927-315-8	Sequence 8, Appli
29	3179	71.6	843	13	US-10-124-598-2	Sequence 2, Appli
30	3179	71.6	843	14	US-10-096-144-2	Sequence 2, Appli
31	3179	71.6	843	14	US-10-190-417-8	Sequence 8, Appli
32	2532.5	57.0	661	10	US-10-246-785-5	Sequence 5, Appli
33	1456.5	32.8	840	10	US-03-361-652-1	Sequence 1, Appli
34	1456.5	32.8	840	10	US-03-927-315-1	Sequence 1, Appli
35	1456.5	32.8	840	14	US-10-246-785-3	Sequence 3, Appli
36	1456.5	32.8	840	14	US-10-190-417-1	Sequence 1, Appli
37	1456.5	32.8	840	14	US-10-159-339-12	Sequence 12, Appli
38	1456.5	32.8	840	14	US-10-179-373-16	Sequence 16, Appli
39	1456.5	32.8	840	15	US-10-436-715-39	Sequence 39, Appli
40	1456.5	32.8	840	15	US-10-436-715-69	Sequence 69, Appli
41	1456.5	32.8	840	16	US-10-725-103-16	Sequence 16, Appli
42	1456.5	32.8	840	16	US-10-725-489-16	Sequence 16, Appli
43	1456.5	32.8	840	16	US-10-725-080A-16	Sequence 16, Appli
44	1456.5	32.8	840	17	US-10-725-472A-16	Sequence 16, Appli
45	1446.5	32.6	842	15	US-10-436-715-35	Sequence 35, Appli

ALIGNMENTS

RESULT 1
US-09-897-427A-4
; Sequence 4, Application US/09897427A
; Patent No. US20020160424A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: LI, XIADONG
; APPLICANT: STAZESKI, LENA
; APPLICANT: XU, HONG
; APPLICANT: EHEVERRI, FERNANDO
; TITLE OF INVENTION: TIR HETERO-OLIGOMERIC TASTE RECEPTORS
; FILE REFERENCE: 078003-0282558
; CURRENT APPLICATION NUMBER: US/09/897,427A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-427A-4

Query Match	100.0%;	Score 4443;	DB 9;	Length 839;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 839;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	MGPRAKTICSLFLLWLAEPAENSDYLPDYLGLGLSLHANMKGIHNLFLQVPMCK	60	
Qy	61	EYEVKVLGYNLMQAMRFAVEINNDSSLLPGVLLGVEIVDVCYISNNVQVFLFLAHEDN	120	
Db	61	EYEVKVLGYNLMQAMRFAVEINNDSSLLPGVLLGVEIVDVCYISNNVQVFLFLAHEDN	120	
Qy	121	LLPQEDYSNYISGRVAVIGPDNSESVMTVANFLSLFLLPQITYSATSDLRDKVRFPAL	180	

Db 121 LLPIQEDYSNYSRVAIVGPDNSSEWMTVANFSLFLLPQITYSAISDELDRKVRPAL 180
 QY 181 LRTTPSADHVEAMVQLMLHFRNWIIVLVSSDTYGRDNGCOLLGERVARDICIAFOETL 240
 Db 181 LRTTPSADHVEAMVQLMLHFRNWIIVLVSSDTYGRDNGCOLLGERVARDICIAFOETL 240
 QY 241 PTLOPNQMTSEERQRLVTIVDKLQOSTARVVVVVFPDGLTYHFFNEVLRFQNTGAVWIA 300
 Db 241 PTLOPNQMTSEERQRLVTIVDKLQOSTARVVVVVFPDGLTYHFFNEVLRFQNTGAVWIA 300
 QY 301 SESWADPVLHNLTELGHGTLGTTITQSVPIPGFSEFRWGPQAGPPPLSRTSQSYTCN 360
 Db 301 SESWADPVLHNLTELGHGTLGTTITQSVPIPGFSEFRWGPQAGPPPLSRTSQSYTCN 360
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 Db 361 QBCDNCNATLSFNTILRLSGRVVYSVAVVAHALHSLGCDKSTCTKRVVWPQL 420
 QY 421 LEEIKVNFLLDHOIFDFDQGVVALHLEIVQWQDRSQNPFPQSVASYYPQLQKNIQD 480
 Db 421 LEEIKVNFLLDHOIFDFDQGVVALHLEIVQWQDRSQNPFPQSVASYYPQLQKNIQD 480
 QY 481 ISWHTVNTTIPMSMCKRQSGQKKPVGIVHCCFECIDCLPGTFLNHTDEYECQACPN 540
 Db 481 ISWHTVNTTIPMSMCKRQSGQKKPVGIVHCCFECIDCLPGTFLNHTDEYECQACPN 540
 QY 541 NEWSYQSETSCFKRQLFLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
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 QY 601 GPMCFMLTLLVAYMVVVPVGPVKYSTCLCRQALPFLCFTTICISCIARSFOIVCAFK 660
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RESULT 2
 US-10-035-045-21
 ; Sequence 21, Application US/10035045
 ; Publication No. US2003005448A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ADLER, JON ELLIOT
 ; APPLICANT: LI, XIAODONG
 ; APPLICANT: STASZEWSKI, LENA
 ; APPLICANT: O'CONNELL, SHAWN
 ; APPLICANT: ZOZULYA, SERGEY
 ; TITLE OF INVENTION: TIR TASTE RECEPTORS AND GENES ENCODING SAME
 ; FILE REFERENCE: 078003-0280681
 ; CURRENT APPLICATION NUMBER: US/10/035,045
 ; CURRENT FILING DATE: 2002-01-03
 ; PRIOR APPLICATION NUMBER: 60/259,227
 ; PRIOR FILING DATE: 2001-01-03
 ; PRIOR APPLICATION NUMBER: 60/284,547
 ; PRIOR FILING DATE: 2001-04-19
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 21
 ; LENGTH: 839
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-035-045-21

Query Match 100.0%; Score 4443; DB 14; Length 839;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGPRAKTIICSLFLLVLAEPASNDPFLPGDYLGLGFLSHANMKGIHVHNFLOVPMCK 60
 Db 1 MGPRAKTIICSLFLLVLAEPASNDPFLPGDYLGLGFLSHANMKGIHVHNFLOVPMCK 60
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 Db 421 LEEIKVNFLLDHOIFDFDQGVVALHLEIVQWQDRSQNPFPQSVASYYPQLQKNIQD 480
 QY 481 ISWHTVNTTIPMSMCKRQSGQKKPVGIVHCCFECIDCLPGTFLNHTDEYECQACPN 540
 Db 481 ISWHTVNTTIPMSMCKRQSGQKKPVGIVHCCFECIDCLPGTFLNHTDEYECQACPN 540
 QY 541 NEWSYQSETSCFKRQLFLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
 Db 541 NEWSYQSETSCFKRQLFLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
 QY 601 GPMCFMLTLLVAYMVVVPVGPVKYSTCLCRQALPFLCFTTICISCIARSFOIVCAFK 660
 Db 601 GPMCFMLTLLVAYMVVVPVGPVKYSTCLCRQALPFLCFTTICISCIARSFOIVCAFK 660
 QY 661 MASRFPRAYSWVRVYQGPVSMAPITVLKMWIVVIGMLATGLSPTTRTDDPKITIVSC 720
 Db 661 MASRFPRAYSWVRVYQGPVSMAPITVLKMWIVVIGMLATGLSPTTRTDDPKITIVSC 720
 QY 721 NPYNRSLLNTSLDILLSVVGFSGFAYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780
 Db 721 NPYNRSLLNTSLDILLSVVGFSGFAYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780
 QY 781 SAYSGVLVTIVDLLVTVLNLLAISLGYPGPKCYMILFYPERNTPAYFNSMIQGYTMRD 839
 Db 781 SAYSGVLVTIVDLLVTVLNLLAISLGYPGPKCYMILFYPERNTPAYFNSMIQGYTMRD 839

RESULT 3
 US-10-179-373-6
 ; Sequence 6, Application US/10179373
 ; Publication No. US20030232407A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZOLLER, MARK
 ; APPLICANT: LI, XIAODONG
 ; APPLICANT: STASZEWSKI, LENA
 ; APPLICANT: O'CONNELL, SHAWN
 ; APPLICANT: ZOZULYA, SERGEY
 ; APPLICANT: ADLER, JON
 ; APPLICANT: XU, HONG

; APPLICANT: ECHEVERRI, FERNANDO
 ; TITLE OF INVENTION: TIR HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES
 ; TITLE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
 ; TITLE OF INVENTION: IDENTIFICATION OF TASTE COMPOUNDS
 ; FILE REFERENCE: 078003-0291566
 ; CURRENT APPLICATION NUMBER: US/10/179,373
 ; PRIOR FILING DATE: 2002-06-26
 ; PRIOR APPLICATION NUMBER: 60/300,434
 ; PRIOR FILING DATE: 2001-06-26
 ; PRIOR APPLICATION NUMBER: 60/304,749
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: 60/310,493
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: 60/331,771
 ; PRIOR FILING DATE: 2001-11-21
 ; PRIOR APPLICATION NUMBER: 60/339,472
 ; PRIOR FILING DATE: 2001-12-14
 ; PRIOR APPLICATION NUMBER: 60/372,090
 ; PRIOR FILING DATE: 2002-04-15
 ; PRIOR APPLICATION NUMBER: 60/374,143
 ; PRIOR FILING DATE: 2002-04-22
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 839
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-179-373-6

Query Match 100.0%; Score 4443; DB 14; Length 839;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGPRAKTICSLFLLWLVAEPAENSDFYLPDYLGLGFLSHANMKGVHNLFLQVPMCK	60
DB	1	MGPRAKTICSLFLLWLVAEPAENSDFYLPDYLGLGFLSHANMKGVHNLFLQVPMCK	60
QY	61	EYEVKVIQYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN	120
DB	61	EYEVKVIQYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN	120
QY	121	LLPIQEDYSNYSIRVAVIGPDNSSEVMTVANFLSLFLPQITYSAISDELKRVFPAL	180
DB	121	LLPIQEDYSNYSIRVAVIGPDNSSEVMTVANFLSLFLPQITYSAISDELKRVFPAL	180
QY	181	LRTTPSADHVEAMVQMLHFRWNWIIIVLSSDTYGRDNGQLLGERVARRDICTAFQETL	240
DB	181	LRTTPSADHVEAMVQMLHFRWNWIIIVLSSDTYGRDNGQLLGERVARRDICTAFQETL	240
QY	241	PTLPQNMNTSEEROLVTIVDKLQOSTARVVVVFSPDLTYHFFNEVLNQFTGAVWIA	300
DB	241	PTLPQNMNTSEEROLVTIVDKLQOSTARVVVVFSPDLTYHFFNEVLNQFTGAVWIA	300
QY	301	SESNAIDPVLNLTGHLGTLGTLTIGTISQVPIPGSEFREWGPQAGPPPLSRTSOSYTCN	360
DB	301	SESNAIDPVLNLTGHLGTLGTLTIGTISQVPIPGSEFREWGPQAGPPPLSRTSOSYTCN	360
QY	361	QECNCLNATISNTILRLSGERVVYVSAYVAHAHLSLLGCDKSTCTKRVVYPWOL	420
DB	361	QECNCLNATISNTILRLSGERVVYVSAYVAHAHLSLLGCDKSTCTKRVVYPWOL	420
QY	421	LEEIMKVNFTLLDHIQIFPDQGDVALHLEIVQWQMDRSONPQSVASYYPQLQKNTQD	480
DB	421	LEEIMKVNFTLLDHIQIFPDQGDVALHLEIVQWQMDRSONPQSVASYYPQLQKNTQD	480
QY	481	ISWHTVNNTPMCMCKKQSQKKKPVGIHVCCPECIDCLPGTFLNHTEDYEYEQACP	540
DB	481	ISWHTVNNTPMCMCKKQSQKKKPVGIHVCCPECIDCLPGTFLNHTEDYEYEQACP	540
QY	541	NEWSQSETSCFKROLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG	600
DB	541	NEWSQSETSCFKROLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG	600

QY	601	GPWCFLMLTLLLVAYMVVVPVYVGPVKVSTCLCRQALFPLCFTICISIAVRSFQIVCAPK	660
DB	601	GPWCFLMLTLLLVAYMVVVPVYVGPVKVSTCLCRQALFPLCFTICISIAVRSFQIVCAPK	660
QY	661	MASRPPRAYSVWRYQGPVSNMAFTIVLKMVIVIGMLATGLSPTRTDPPDKITIVSC	720
DB	661	MASRPPRAYSVWRYQGPVSNMAFTIVLKMVIVIGMLATGLSPTRTDPPDKITIVSC	720
QY	721	NPVNSLLENTSLDLSLVVGFSPAYMKGELPTNNYNAKFTILSMYFTSSVSLCTFM	780
DB	721	NPVNSLLENTSLDLSLVVGFSPAYMKGELPTNNYNAKFTILSMYFTSSVSLCTFM	780
QY	781	SAYSGVLVTIVDLSLVVNLNLAISLGYGPKCYMILFYPERNTPAYFNSMIQGYTMRD	839
DB	781	SAYSGVLVTIVDLSLVVNLNLAISLGYGPKCYMILFYPERNTPAYFNSMIQGYTMRD	839

RESULT 4

US-10-725-103-6
 ; Sequence 6, Application US/10725103
 ; Publication No. US20040175792A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZOLLER, MARK
 ; APPLICANT: LI, XIAODONG
 ; APPLICANT: STRASZESKI, LENA
 ; APPLICANT: O'CONNELL, SHAWN
 ; APPLICANT: ZOZULYA, SERGEY
 ; APPLICANT: ADLER, JON
 ; APPLICANT: XU, HONG
 ; APPLICANT: ECHEVERRI, FERNANDO
 ; TITLE OF INVENTION: TIR HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES
 ; TITLE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
 ; TITLE OF INVENTION: IDENTIFICATION OF TASTE COMPOUNDS
 ; FILE REFERENCE: 078003-0291566
 ; CURRENT APPLICATION NUMBER: US/10/725,103
 ; CURRENT FILING DATE: 2003-12-02
 ; PRIOR APPLICATION NUMBER: 60/300,434
 ; PRIOR FILING DATE: 2001-06-26
 ; PRIOR APPLICATION NUMBER: 60/304,749
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: 60/310,493
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: 60/331,771
 ; PRIOR FILING DATE: 2001-11-21
 ; PRIOR APPLICATION NUMBER: 60/339,472
 ; PRIOR FILING DATE: 2001-12-14
 ; PRIOR APPLICATION NUMBER: 60/372,090
 ; PRIOR FILING DATE: 2002-04-15
 ; PRIOR APPLICATION NUMBER: 60/374,143
 ; PRIOR FILING DATE: 2002-04-22
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 839
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-725-103-6

Query Match 100.0%; Score 4443; DB 16; Length 839;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGPRAKTICSLFLLWLVAEPAENSDFYLPDYLGLGFLSHANMKGVHNLFLQVPMCK	60
DB	1	MGPRAKTICSLFLLWLVAEPAENSDFYLPDYLGLGFLSHANMKGVHNLFLQVPMCK	60
QY	61	EYEVKVIQYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN	120
DB	61	EYEVKVIQYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN	120
QY	121	LLPIQEDYSNYSIRVAVIGPDNSSEVMTVANFLSLFLPQITYSAISDELKRVFPAL	180
DB	121	LLPIQEDYSNYSIRVAVIGPDNSSEVMTVANFLSLFLPQITYSAISDELKRVFPAL	180

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QY 181 LRTTPADHVEAMVQLMLHFRWNIIIVSSDTYGRDNGQLLGERVARRDICIATFOTL 240
Db 181 LRTTPADHVEAMVQLMLHFRWNIIIVSSDTYGRDNGQLLGERVARRDICIATFOTL 240
QY 241 PTLOPNQMTSEERQRLVTIVDKLQOSTARVVVVVSPDLTYHFFNEVLNQFTGAVWIA 300
Db 241 PTLOPNQMTSEERQRLVTIVDKLQOSTARVVVVVSPDLTYHFFNEVLNQFTGAVWIA 300
QY 301 SESWADPVLHNLTELGHGTFGLGITIQSVPIPGFSEFREWGPQAGPPPLSRSTSOSYTCN 360
Db 301 SESWADPVLHNLTELGHGTFGLGITIQSVPIPGFSEFREWGPQAGPPPLSRSTSOSYTCN 360
QY 361 QECNCLNATLSFNTILRLSERVVVSVYSAVAVAHALHSLGCDKSTCTKRVVYVWQL 420
Db 361 QECNCLNATLSFNTILRLSERVVVSVYSAVAVAHALHSLGCDKSTCTKRVVYVWQL 420
QY 421 LEEIKVNFLLDHQIFPDQGDVALHLEIVQWQDRSQNPFSQSVASYYPFLQRLKNIQD 480
Db 421 LEEIKVNFLLDHQIFPDQGDVALHLEIVQWQDRSQNPFSQSVASYYPFLQRLKNIQD 480
QY 481 ISWHTVNNNTIPMSMCKRCSQSGQKKPVGHVCCFECIDCLPGTFLNHTDEYECQACPN 540
Db 481 ISWHTVNNNTIPMSMCKRCSQSGQKKPVGHVCCFECIDCLPGTFLNHTDEYECQACPN 540
QY 541 NEWSYQSETSCFKRQLVFLWEHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
Db 541 NEWSYQSETSCFKRQLVFLWEHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
QY 601 GPMCFLMLTLLVAVMVVVPVGVGPKYSTCLCROALPPLCFTICISCIIVRSFQIVCAFK 660
Db 601 GPMCFLMLTLLVAVMVVVPVGVGPKYSTCLCROALPPLCFTICISCIIVRSFQIVCAFK 660
QY 661 MASRFPRAYSVWRYQGPVYSMAFITVLKMWIVVIGMLATGLSTTRTDDPKITIVSC 720
Db 661 MASRFPRAYSVWRYQGPVYSMAFITVLKMWIVVIGMLATGLSTTRTDDPKITIVSC 720
QY 721 NPYNRSLLENFTSLDILLVSVGFSAVYKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780
Db 721 NPYNRSLLENFTSLDILLVSVGFSAVYKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780
QY 781 SAYSGVLVTIVDLLVTVNLNLAISLGYPGPKCYMILFYPERNTPAYFNSMIQGYTMRD 839
Db 781 SAYSGVLVTIVDLLVTVNLNLAISLGYPGPKCYMILFYPERNTPAYFNSMIQGYTMRD 839

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RESULT 5
US-10-725-489-6
; Sequence 6, Application US/10725489
; Publication No. US2004017593A1
; GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK
; APPLICANT: LI, XIAODONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: ADLER, JON
; APPLICANT: XU, HONG
; APPLICANT: ECHEVERRI, FERNANDO
; TITLE OF INVENTION: TIR HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES
; TITLE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
; TITLE OF INVENTION: IDENTIFICATION OF TASTE COMPOUNDS
; FILE REFERENCE: 078003-0291566
; CURRENT APPLICATION NUMBER: US/10725, 489
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/300, 434
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/304, 749
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/310, 493
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/331, 771
; PRIOR FILING DATE: 2001-11-21

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; PRIOR APPLICATION NUMBER: 60/339, 472
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/372, 090
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/374, 143
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-725-489-6

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Query Match 100.0%; Score 4443; DB 16; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPRAKTICSLFLLVLAEPANSDFYLPDGLGFLSLHANMKGIVHLNFIQVPMCK 60
Db 1 MGPRAKTICSLFLLVLAEPANSDFYLPDGLGFLSLHANMKGIVHLNFIQVPMCK 60
QY 61 EYEVKVTGYNLMQAMPFAVEEINNDSSLLPGVLLGYEIVDVCIYISNNVQVLYFLAHDN 120
Db 61 EYEVKVTGYNLMQAMPFAVEEINNDSSLLPGVLLGYEIVDVCIYISNNVQVLYFLAHDN 120
QY 121 LLPTQEDYSNYISRWAVIGPDNSESVMTVANFLSLFLLPQITVYSALSDLRKVRFPAL 180
Db 121 LLPTQEDYSNYISRWAVIGPDNSESVMTVANFLSLFLLPQITVYSALSDLRKVRFPAL 180
QY 181 LRTTPADHVEAMVQLMLHFRWNIIIVSSDTYGRDNGQLLGERVARRDICIATFOTL 240
Db 181 LRTTPADHVEAMVQLMLHFRWNIIIVSSDTYGRDNGQLLGERVARRDICIATFOTL 240
QY 241 PTLOPNQMTSEERQRLVTIVDKLQOSTARVVVVVSPDLTYHFFNEVLNQFTGAVWIA 300
Db 241 PTLOPNQMTSEERQRLVTIVDKLQOSTARVVVVVSPDLTYHFFNEVLNQFTGAVWIA 300
QY 301 SESWADPVLHNLTELGHGTFGLGITIQSVPIPGFSEFREWGPQAGPPPLSRSTSOSYTCN 360
Db 301 SESWADPVLHNLTELGHGTFGLGITIQSVPIPGFSEFREWGPQAGPPPLSRSTSOSYTCN 360
QY 361 QECNCLNATLSFNTILRLSERVVVSVYSAVAVAHALHSLGCDKSTCTKRVVYVWQL 420
Db 361 QECNCLNATLSFNTILRLSERVVVSVYSAVAVAHALHSLGCDKSTCTKRVVYVWQL 420
QY 421 LEEIKVNFLLDHQIFPDQGDVALHLEIVQWQDRSQNPFSQSVASYYPFLQRLKNIQD 480
Db 421 LEEIKVNFLLDHQIFPDQGDVALHLEIVQWQDRSQNPFSQSVASYYPFLQRLKNIQD 480
QY 481 ISWHTVNNNTIPMSMCKRCSQSGQKKPVGHVCCFECIDCLPGTFLNHTDEYECQACPN 540
Db 481 ISWHTVNNNTIPMSMCKRCSQSGQKKPVGHVCCFECIDCLPGTFLNHTDEYECQACPN 540
QY 541 NEWSYQSETSCFKRQLVFLWEHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
Db 541 NEWSYQSETSCFKRQLVFLWEHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
QY 601 GPMCFLMLTLLVAVMVVVPVGVGPKYSTCLCROALPPLCFTICISCIIVRSFQIVCAFK 660
Db 601 GPMCFLMLTLLVAVMVVVPVGVGPKYSTCLCROALPPLCFTICISCIIVRSFQIVCAFK 660
QY 661 MASRFPRAYSVWRYQGPVYSMAFITVLKMWIVVIGMLATGLSTTRTDDPKITIVSC 720
Db 661 MASRFPRAYSVWRYQGPVYSMAFITVLKMWIVVIGMLATGLSTTRTDDPKITIVSC 720
QY 721 NPYNRSLLENFTSLDILLVSVGFSAVYKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780
Db 721 NPYNRSLLENFTSLDILLVSVGFSAVYKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780
QY 781 SAYSGVLVTIVDLLVTVNLNLAISLGYPGPKCYMILFYPERNTPAYFNSMIQGYTMRD 839
Db 781 SAYSGVLVTIVDLLVTVNLNLAISLGYPGPKCYMILFYPERNTPAYFNSMIQGYTMRD 839

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RESULT 6
US-10-725-080A-6
; Sequence 6, Application US/10725080A
; Publication No. US20040185469A1
; GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK
; APPLICANT: LI, XIAODONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: ADLER, JON
; APPLICANT: XU, HONG
; APPLICANT: ECHEVERRI, FERNANDO
; TITLE OF INVENTION: TIR HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES
; TITLE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
; TITLE OF INVENTION: IDENTIFICATION OF TASTE COMPOUNDS
; FILE REFERENCE: 078003-0291566
; CURRENT APPLICATION NUMBER: US/10/725,080A
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/300,434
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/304,749
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/310,493
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/331,771
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/339,472
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/372,090
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/374,143
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-725-080A-6

Query Match 100.0%; Score 4443; DB 16; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPRAKTICSLFLLWVLAEPANSDFYLPDGYLLGGLFSLHANMKGIVHLNFIQVPMCK 60
DB 1 MGPRAKTICSLFLLWVLAEPANSDFYLPDGYLLGGLFSLHANMKGIVHLNFIQVPMCK 60
QY 61 EYEVKVIQYNLMQAMRFAVEEINDDSLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN 120
DB 61 EYEVKVIQYNLMQAMRFAVEEINDDSLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN 120
QY 121 LLPIQEDYSNYSIRVAVIGPNDSVMTVANFLSLFLPQITYSAISDELARDKVRFPAL 180
DB 121 LLPIQEDYSNYSIRVAVIGPNDSVMTVANFLSLFLPQITYSAISDELARDKVRFPAL 180
QY 181 LRTTPSADHVEAMVQLMLHFRWNIIIVLSDDTYGRNGQLLGBRVARRDICIAFQETL 240
DB 181 LRTTPSADHVEAMVQLMLHFRWNIIIVLSDDTYGRNGQLLGBRVARRDICIAFQETL 240
QY 241 PTLQPNQNTSERORLVTIVDKQOSTARVVVVFSPDLTLHFFNEVLNQFTGAVIA 300
DB 241 PTLQPNQNTSERORLVTIVDKQOSTARVVVVFSPDLTLHFFNEVLNQFTGAVIA 300
QY 301 SESWAIDPVLHNLTELGHTFLGITIQSVPIPGFSEFREMGPQAGPPPLSRTSQTNC 360
DB 301 SESWAIDPVLHNLTELGHTFLGITIQSVPIPGFSEFREMGPQAGPPPLSRTSQTNC 360
QY 361 QECNCLNATLSFNTILRSGRVVYVSVYAVAHALHSLGCDKSTCTKRVVYPMQL 420

DB 361 QECNCLNATLSFNTILRSGRVVYVSVYAVAHALHSLGCDKSTCTKRVVYPMQL 420
QY 421 LEEITWKVNFTLLDHOIFPDPOGDVALHLEIYVQWQDRSONPQSVASYPLQRLQKNIQD 480
DB 421 LEEITWKVNFTLLDHOIFPDPOGDVALHLEIYVQWQDRSONPQSVASYPLQRLQKNIQD 480
QY 481 ISWHTVNNNTIPMSMCKSCQSGQKKKPVGIHVCCFECIDCLPGTFLNHTEDYEYEQACFN 540
DB 481 ISWHTVNNNTIPMSMCKSCQSGQKKKPVGIHVCCFECIDCLPGTFLNHTEDYEYEQACFN 540
QY 541 NEWSYQSETSCFKQLVFLWEHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
DB 541 NEWSYQSETSCFKQLVFLWEHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
QY 601 GPMCFMLTLLVAYVMVVPVYVGPVKSTCLCRQALFPLCFTICISCIAVRSFQIVCAFK 660
DB 601 GPMCFMLTLLVAYVMVVPVYVGPVKSTCLCRQALFPLCFTICISCIAVRSFQIVCAFK 660
QY 661 MASRFPRAYSYVRYQGPVYSMAFITVLKMWIVVIGMLATGLSPTRTDPPDKITIVSC 720
DB 661 MASRFPRAYSYVRYQGPVYSMAFITVLKMWIVVIGMLATGLSPTRTDPPDKITIVSC 720
QY 721 NPYNRSLLFNTSLDLLSVVGFSPAYMGKELPTNNEAKFITLSMTFYFTSSVSLCTFM 780
DB 721 NPYNRSLLFNTSLDLLSVVGFSPAYMGKELPTNNEAKFITLSMTFYFTSSVSLCTFM 780
QY 781 SAYSGVLVTIVDLLVTVLNLLAISLGYGPKCYMILFYPERNTPAYFNMSIQGYTMRD 839
DB 781 SAYSGVLVTIVDLLVTVLNLLAISLGYGPKCYMILFYPERNTPAYFNMSIQGYTMRD 839

RESULT 7
US-10-725-472A-6
; Sequence 6, Application US/10725472A
; Publication No. US20040191862A1
; GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK
; APPLICANT: LI, XIAODONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: ADLER, JON
; APPLICANT: XU, HONG
; APPLICANT: ECHEVERRI, FERNANDO
; TITLE OF INVENTION: TIR HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES
; TITLE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
; TITLE OF INVENTION: IDENTIFICATION OF TASTE COMPOUNDS
; FILE REFERENCE: 078003-0291566
; CURRENT APPLICATION NUMBER: US/10/725,472A
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/300,434
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/304,749
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/310,493
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/331,771
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/339,472
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/372,090
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/374,143
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-725-472A-6

Query Match 100.0%; Score 4443; DB 17; Length 839;

```

Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGPRAKTICSLFLLWLAEPANSDYLPDGLGGLFSLHANMKGIVHLNFIQVPMCK 60
Db 1 MGPRAKTICSLFLLWLAEPANSDYLPDGLGGLFSLHANMKGIVHLNFIQVPMCK 60
Qy 61 EYEVKVIQYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQVLYFLAHDN 120
Db 61 EYEVKVIQYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQVLYFLAHDN 120
Qy 121 LLPTQEDYSNYSRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRKVRFPAL 180
Db 121 LLPTQEDYSNYSRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRKVRFPAL 180
Qy 181 LRTTPSADHVEAMVQMLHFRWNIIIVLSSDTYGRDNGQLLGERVARRDICIAPQETL 240
Db 181 LRTTPSADHVEAMVQMLHFRWNIIIVLSSDTYGRDNGQLLGERVARRDICIAPQETL 240
Qy 241 PTLOPNQMTSEERQRLVTIVDKLQOSTARVVVVSFDPDLTYHFFNEVLRQNFAGVWIA 300
Db 241 PTLOPNQMTSEERQRLVTIVDKLQOSTARVVVVSFDPDLTYHFFNEVLRQNFAGVWIA 300
Qy 301 SESWAIDPVHLNLTGHLGTLGTLGITIQSVPIPGFSEFREWGPQAGPPPLSRTSQTCTN 360
Db 301 SESWAIDPVHLNLTGHLGTLGTLGITIQSVPIPGFSEFREWGPQAGPPPLSRTSQTCTN 360
Qy 361 QECNCLNATLSFNTILRLSGERVVYSYAVAVAHALSHLLGCDKSTCTKRVVYVWQL 420
Db 361 QECNCLNATLSFNTILRLSGERVVYSYAVAVAHALSHLLGCDKSTCTKRVVYVWQL 420
Qy 421 LEEIWKVNFLLDHOIFPDQGVVALHLEIVQWQDRSQNPFGQSVASYYPQLQOLKNIQD 480
Db 421 LEEIWKVNFLLDHOIFPDQGVVALHLEIVQWQDRSQNPFGQSVASYYPQLQOLKNIQD 480
Qy 481 ISWHTVNTTIPMSCKRQSGQKKPVGIHVCCFECIDCLPGTFLNHTEDYECCQACPN 540
Db 481 ISWHTVNTTIPMSCKRQSGQKKPVGIHVCCFECIDCLPGTFLNHTEDYECCQACPN 540
Qy 541 NEWSQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
Db 541 NEWSQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
Qy 601 GPMCFMLTLLVAYMVVYVGPVSTCLCRQALPFLCTICISCIASVRSFOIVCAFK 660
Db 601 GPMCFMLTLLVAYMVVYVGPVSTCLCRQALPFLCTICISCIASVRSFOIVCAFK 660
Qy 661 MASRFPRAYSYVWRYQGPVYSMAFITVLKMWIVVIGMLATGLSPTRTDDPKITIVSC 720
Db 661 MASRFPRAYSYVWRYQGPVYSMAFITVLKMWIVVIGMLATGLSPTRTDDPKITIVSC 720
Qy 721 NPYNRSLLNTSLDLSLVVGSFAYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780
Db 721 NPYNRSLLNTSLDLSLVVGSFAYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780
Qy 781 SAYSGVLVTIVDLSLVVNLALSLGYFGPKCYMILFYPERNTPAYFNMSIQGYTMRD 839
Db 781 SAYSGVLVTIVDLSLVVNLALSLGYFGPKCYMILFYPERNTPAYFNMSIQGYTMRD 839

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RESULT 8

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US-10-725-276-21
; Sequence 21, Application US/10725276
; Publication No. US20040209286A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: LI, XIAODONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: ZOULYA, SERGEY
; TITLE OF INVENTION: TIR TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003-0280681
; CURRENT APPLICATION NUMBER: US/10/725,276

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; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/259,227
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 60/284,547
; PRIOR FILING DATE: 2001-04-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-725-276-21

```

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Query Match 100.0%; Score 4443; DB 17; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MGPRAKTICSLFLLWLAEPANSDYLPDGLGGLFSLHANMKGIVHLNFIQVPMCK 60
Db 1 MGPRAKTICSLFLLWLAEPANSDYLPDGLGGLFSLHANMKGIVHLNFIQVPMCK 60
Qy 61 EYEVKVIQYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQVLYFLAHDN 120
Db 61 EYEVKVIQYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQVLYFLAHDN 120
Qy 121 LLPTQEDYSNYSRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRKVRFPAL 180
Db 121 LLPTQEDYSNYSRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRKVRFPAL 180
Qy 181 LRTTPSADHVEAMVQMLHFRWNIIIVLSSDTYGRDNGQLLGERVARRDICIAPQETL 240
Db 181 LRTTPSADHVEAMVQMLHFRWNIIIVLSSDTYGRDNGQLLGERVARRDICIAPQETL 240
Qy 241 PTLOPNQMTSEERQRLVTIVDKLQOSTARVVVVSFDPDLTYHFFNEVLRQNFAGVWIA 300
Db 241 PTLOPNQMTSEERQRLVTIVDKLQOSTARVVVVSFDPDLTYHFFNEVLRQNFAGVWIA 300
Qy 301 SESWAIDPVHLNLTGHLGTLGTLGITIQSVPIPGFSEFREWGPQAGPPPLSRTSQTCTN 360
Db 301 SESWAIDPVHLNLTGHLGTLGTLGITIQSVPIPGFSEFREWGPQAGPPPLSRTSQTCTN 360
Qy 361 QECNCLNATLSFNTILRLSGERVVYSYAVAVAHALSHLLGCDKSTCTKRVVYVWQL 420
Db 361 QECNCLNATLSFNTILRLSGERVVYSYAVAVAHALSHLLGCDKSTCTKRVVYVWQL 420
Qy 421 LEEIWKVNFLLDHOIFPDQGVVALHLEIVQWQDRSQNPFGQSVASYYPQLQOLKNIQD 480
Db 421 LEEIWKVNFLLDHOIFPDQGVVALHLEIVQWQDRSQNPFGQSVASYYPQLQOLKNIQD 480
Qy 481 ISWHTVNTTIPMSCKRQSGQKKPVGIHVCCFECIDCLPGTFLNHTEDYECCQACPN 540
Db 481 ISWHTVNTTIPMSCKRQSGQKKPVGIHVCCFECIDCLPGTFLNHTEDYECCQACPN 540
Qy 541 NEWSQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
Db 541 NEWSQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
Qy 601 GPMCFMLTLLVAYMVVYVGPVSTCLCRQALPFLCTICISCIASVRSFOIVCAFK 660
Db 601 GPMCFMLTLLVAYMVVYVGPVSTCLCRQALPFLCTICISCIASVRSFOIVCAFK 660
Qy 661 MASRFPRAYSYVWRYQGPVYSMAFITVLKMWIVVIGMLATGLSPTRTDDPKITIVSC 720
Db 661 MASRFPRAYSYVWRYQGPVYSMAFITVLKMWIVVIGMLATGLSPTRTDDPKITIVSC 720
Qy 721 NPYNRSLLNTSLDLSLVVGSFAYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780
Db 721 NPYNRSLLNTSLDLSLVVGSFAYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780
Qy 781 SAYSGVLVTIVDLSLVVNLALSLGYFGPKCYMILFYPERNTPAYFNMSIQGYTMRD 839
Db 781 SAYSGVLVTIVDLSLVVNLALSLGYFGPKCYMILFYPERNTPAYFNMSIQGYTMRD 839

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RESULT 9
US-10-770-127-198
; Sequence 198, Application US/10770127
; Publication No. US20040214239A1
; GENERAL INFORMATION:
; APPLICANT: SERVANT, GUY
; APPLICANT: OZECK, MARK
; APPLICANT: BRUST, PAUL
; APPLICANT: XU, HONG
; TITLE OF INVENTION: FUNCTIONAL COUPLING OF TIRS AND T2RS BY GI PROTEINS
; TITLE OF INVENTION: AND CELL-BASED ASSAYS FOR THE IDENTIFICATION OF TIR
; TITLE OF INVENTION: AND T2R MODULATORS
; FILE REFERENCE: 100337.54281US
; CURRENT APPLICATION NUMBER: US/10/770,127
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: 60/444,172
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 60/457,318
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 198
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-127-198

Query Match      100.0%; Score 4443; DB 17; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPRAKTICSLFLLWLVAEPAENSDFYLPDGYLLGGLFSLHANNKGIVHLNFIQVPMCK 60
DB 1 MGPRAKTICSLFLLWLVAEPAENSDFYLPDGYLLGGLFSLHANNKGIVHLNFIQVPMCK 60
QY 61 EYEVKVI GYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVYISNNVQPVLYFLAHEDN 120
DB 61 EYEVKVI GYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVYISNNVQPVLYFLAHEDN 120
QY 121 LLPTQEDYSNYSIRVAVIGPDNSESVMVANFSLFLLPQITYSASIDELRDKVRFPAL 180
DB 121 LLPTQEDYSNYSIRVAVIGPDNSESVMVANFSLFLLPQITYSASIDELRDKVRFPAL 180
QY 181 LRTTPSADHVEAMVQMLHFRWNWIIVLVSSDTYGRDNGQLGERVARRDICIATFQETL 240
DB 181 LRTTPSADHVEAMVQMLHFRWNWIIVLVSSDTYGRDNGQLGERVARRDICIATFQETL 240
QY 241 PTLQPNQMTSEERQRLVTIIVDKLQOSTARVVVVVSPDLTYLHFNEVLRQNTGAVWIA 300
DB 241 PTLQPNQMTSEERQRLVTIIVDKLQOSTARVVVVVSPDLTYLHFNEVLRQNTGAVWIA 300
QY 301 SESWAIDPVLHNLTELGHGLTFLGTTIOSVPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360
DB 301 SESWAIDPVLHNLTELGHGLTFLGTTIOSVPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360
QY 361 QECNCLNATLSFNTILRLSGERVYVYSYAVAVAHALSHLGCCKSTCTKRVVYPWQL 420
DB 361 QECNCLNATLSFNTILRLSGERVYVYSYAVAVAHALSHLGCCKSTCTKRVVYPWQL 420
QY 421 LEEIWKVNFTLLDHIQIFPDQGDVALHLEIVQWQDRSQNPFSQSVASYPLQRLQKNIQD 480
DB 421 LEEIWKVNFTLLDHIQIFPDQGDVALHLEIVQWQDRSQNPFSQSVASYPLQRLQKNIQD 480
QY 481 ISWHTVNNITPMSCKSKCQSQGKKKPVGIHVCCPECIDCLPGTFLNHTEDYEBCQCPN 540
DB 481 ISWHTVNNITPMSCKSKCQSQGKKKPVGIHVCCPECIDCLPGTFLNHTEDYEBCQCPN 540
QY 541 NEWSQOSTSCFKROLVLEWHEAPTIIVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
DB 541 NEWSQOSTSCFKROLVLEWHEAPTIIVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
QY 601 GPMCFLMTLLLVAYMVVVPVGVKSTCLCRQALFPLCTICISCIASVRSFQIVCAFK 660

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DB 601 GPMCFLMTLLLVAYMVVVPVGVKSTCLCRQALFPLCTICISCIASVRSFQIVCAFK 660
QY 661 MASRPPRAYSWVRYOQPYVSMAFITVLKMWIVVIGMLATGLSPTRTDDPKKITIVSC 720
DB 661 MASRPPRAYSWVRYOQPYVSMAFITVLKMWIVVIGMLATGLSPTRTDDPKKITIVSC 720
QY 721 NPVNRSLPNTSLDLSLLSVVGFSPAYMGKELPNYNEAKFITLSMTFYFTSSVSLCTFM 780
DB 721 NPVNRSLPNTSLDLSLLSVVGFSPAYMGKELPNYNEAKFITLSMTFYFTSSVSLCTFM 780
QY 781 SAYSGVLVTIIVDLLAVTVLNLALISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRD 839
DB 781 SAYSGVLVTIIVDLLAVTVLNLALISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRD 839

RESULT 10
US-10-246-785-4
; Sequence 4, Application US/10246785
; Publication No. US2003014848A1
; GENERAL INFORMATION:
; APPLICANT: IRM, LLC
; APPLICANT: The Scripps Research Institute
; APPLICANT: Liao, Jiayu
; APPLICANT: Sheng, Ding
; APPLICANT: Schultz, Peter G
; TITLE OF INVENTION: Sweet Taste Receptors
; FILE REFERENCE: 36-002810US/PC
; CURRENT APPLICATION NUMBER: US/10/246,785
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/323,450
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-246-785-4

Query Match      99.5%; Score 4422; DB 14; Length 839;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 834; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGPRAKTICSLFLLWLVAEPAENSDFYLPDGYLLGGLFSLHANNKGIVHLNFIQVPMCK 60
DB 1 MGPRAKTICSLFLLWLVAEPAENSDFYLPDGYLLGGLFSLHANNKGIVHLNFIQVPMCK 60
QY 61 EYEVKVI GYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVYISNNVQPVLYFLAHEDN 120
DB 61 EYEVKVI GYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVYISNNVQPVLYFLAHEDN 120
QY 121 LLPTQEDYSNYSIRVAVIGPDNSESVMVANFSLFLLPQITYSASIDELRDKVRFPAL 180
DB 121 LLPTQEDYSNYSIRVAVIGPDNSESVMVANFSLFLLPQITYSASIDELRDKVRFPAL 180
QY 181 LRTTPSADHVEAMVQMLHFRWNWIIVLVSSDTYGRDNGQLGERVARRDICIATFQETL 240
DB 181 LRTTPSADHVEAMVQMLHFRWNWIIVLVSSDTYGRDNGQLGERVARRDICIATFQETL 240
QY 241 PTLQPNQMTSEERQRLVTIIVDKLQOSTARVVVVVSPDLTYLHFNEVLRQNTGAVWIA 300
DB 241 PTLQPNQMTSEERQRLVTIIVDKLQOSTARVVVVVSPDLTYLHFNEVLRQNTGAVWIA 300
QY 301 SESWAIDPVLHNLTELGHGLTFLGTTIOSVPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360
DB 301 SESWAIDPVLHNLTELGHGLTFLGTTIOSVPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360
QY 361 QECNCLNATLSFNTILRLSGERVYVYSYAVAVAHALSHLGCCKSTCTKRVVYPWQL 420
DB 361 QECNCLNATLSFNTILRLSGERVYVYSYAVAVAHALSHLGCCKSTCTKRVVYPWQL 420
QY 421 LEEIWKVNFTLLDHIQIFPDQGDVALHLEIVQWQDRSQNPFSQSVASYPLQRLQKNIQD 480

```

Db 421 LEEIWKVNFLLDHOIFDPPQGDVALHLEIVQWDRSQNPFOVSASYPLQRLKNIQD 480
 QY 481 ISWHTVNTIPMSKRCQSGOKKPVGHVCCFECIDCLPGTFLNHTDEYEQACPN 540
 Db 481 ISWHTVNTIPMSKRCQSGOKKPVGHVCCFECIDCLPGTFLNHTDEYEQACPN 540
 QY 541 NEWSYQSETSCFKRQLVFLWEHAPTIAVALLAALGFLSLTALIVFWRHFOPTIVRSAG 600
 Db 541 NEWSYQSETSCFKRQLVFLWEHAPTIAVALLAALGFLSLTALIVFWRHFOPTIVRSAG 600
 QY 601 GPMCFMLTLLLVAYMVVPPVGVSTCLCQALFPLCFTTICISCIARSQIVCAFK 660
 Db 601 GPMCFMLTLLLVAYMVVPPVGVSTCLCQALFPLCFTTICISCIARSQIVCAFK 660
 QY 661 MASRFPRAYSYWRVYQGPVSMAPITVLKMWIVVIGMLATGLSPTTRTDDPKITIVSC 720
 Db 661 MASRFPRAYSYWRVYQGPVSMAPITVLKMWIVVIGMLATGLSPTTRTDDPKITIVSC 720
 QY 721 NPNYRSLFNTSLDILLSVVGFSAFYMKGELPTNYNEAKFITLSMTFFYFTSSVSLCTFM 780
 Db 721 NPNYRSLFNTSLDILLSVVGFSAFYMKGELPTNYNEAKFITLSMTFFYFTSSVSLCTFM 780
 QY 781 SAYSGVLVTIVDLLVTNLALISLGYFGPKCYMILFYPERNTPAYFNSMIQYTWRRD 839
 Db 781 SAYSGVLVTIVDLLVTNLALISLGYFGPKCYMILFYPERNTPAYFNSMIQYTWRRD 839

RESULT 11

US-09-927-315-9
 ; Sequence 9, Application US/09927315
 ; Publication No. US20030040045A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zuker, Charles S.
 ; APPLICANT: Ryba, Nicholas J. P.
 ; APPLICANT: Nelson, Greg
 ; APPLICANT: Hoon, Mark A.
 ; APPLICANT: Chandrashekar, Jayaram
 ; APPLICANT: Zhang, Yifeng
 ; APPLICANT: The Regents of the University of California
 ; APPLICANT: The Government of the United States of America
 ; APPLICANT: as represented by the Secretary of the
 ; APPLICANT: Department of Health and Human Services
 ; TITLE OF INVENTION: Mammalian Sweet Taste Receptors
 ; FILE REFERENCE: 02307E-120110US
 ; CURRENT APPLICATION NUMBER: US/09/927,315
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: US 60/302,898
 ; PRIOR FILING DATE: 2001-07-03
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 9
 ; LENGTH: 838
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human T1R2 sweet taste receptor
 US-09-927-315-9

Query Match 98.9%; Score 4392.5; DB 10; Length 838;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 833; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
 QY 1 MGPRATICSFLFWLWLAEPANSDYLPQDYLGLGFLSHANMKGIVHLNFIQVPMCK 60
 Db 1 MGPRATICSFLFWLWLAEPANSDYLPQDYLGLGFLSHANMKGIVHLNFIQVPMCK 60
 QY 61 EYEKVTGYNLMQAMRFAVEINNDSSLLPGVLGYEIVDVCYISNNVQVLYFLAHEDN 120
 Db 61 EYEKVTGYNLMQAMRFAVEINNDSSLLPGVLGYEIVDVCYISNNVQVLYFLAHEDN 120
 QY 121 LLPQEDYSNYISRVVAVIGPDNSESVMTVANFLSLFPQITYSAISDELROKVRPAL 180

Db 121 LLPQEDYSNYISRVVAVIGPDNSESVMTVANFLSLFPQITYSAISDELROKVRPAL 180
 QY 181 LRTTPSADHHVEAMVQLMLHFRWNWIIIVLVSSDTYGRDNGQLLGERVARDICIAFOETL 240
 Db 181 LRTTPSADHHVEAMVQLMLHFRWNWIIIVLVSSDTYGRDNGQLLGERVARDICIAFOETL 240
 QY 241 PTLQPNQNTSEERQRLVTIVDKLOOSTARVVVVVPSDLTYHFFNEVLNQFTGAVWIA 300
 Db 241 PTLQPNQNTSEERQRLVTIVDKLOOSTARVVVVVPSDLTYHFFNEVLNQFTGAVWIA 300
 QY 301 SESWAIDPVLHNLTELGHTFLGITIIOQVPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360
 Db 301 SESWAIDPVLHNLTELGHTFLGITIIOQVPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360
 QY 361 QECNCLNATLSFNTILRLSGERVVSVYSAVAHALHSLGCDKSTCTKRVVWPQL 420
 Db 361 QECNCLNATLSFNTILRLSGERVVSVYSAVAHALHSLGCDKSTCTKRVVWPQL 420
 QY 421 LEEIWKVNFLLDHOIFDPPQGDVALHLEIVQWDRSQNPFOVSASYPLQRLKNIQD 480
 Db 421 LEEIWKVNFLLDHOIFDPPQGDVALHLEIVQWDRSQNPFOVSASYPLQRLKNIQD 480
 QY 481 ISWHTVNTIPMSKRCQSGOKKPVGHVCCFECIDCLPGTFLNHTDEYEQACPN 540
 Db 481 ISWHTVNTIPMSKRCQSGOKKPVGHVCCFECIDCLPGTFLNHTDEYEQACPN 540
 QY 541 NEWSYQSETSCFKRQLVFLWEHAPTIAVALLAALGFLSLTALIVFWRHFOPTIVRSAG 600
 Db 541 NEWSYQSETSCFKRQLVFLWEHAPTIAVALLAALGFLSLTALIVFWRHFOPTIVRSAG 600
 QY 601 GPMCFMLTLLLVAYMVVPPVGVSTCLCQALFPLCFTTICISCIARSQIVCAFK 660
 Db 601 GPMCFMLTLLLVAYMVVPPVGVSTCLCQALFPLCFTTICISCIARSQIVCAFK 660
 QY 661 MASRFPRAYSYWRVYQGPVSMAPITVLKMWIVVIGMLATGLSPTTRTDDPKITIVSC 720
 Db 661 MASRFPRAYSYWRVYQGPVSMAPITVLKMWIVVIGMLATGLSPTTRTDDPKITIVSC 720
 QY 721 NPNYRSLFNTSLDILLSVVGFSAFYMKGELPTNYNEAKFITLSMTFFYFTSSVSLCTFM 780
 Db 721 NPNYRSLFNTSLDILLSVVGFSAFYMKGELPTNYNEAKFITLSMTFFYFTSSVSLCTFM 780
 QY 781 SAYSGVLVTIVDLLVTNLALISLGYFGPKCYMILFYPERNTPAYFNSMIQYTWRRD 839
 Db 781 SAYSGVLVTIVDLLVTNLALISLGYFGPKCYMILFYPERNTPAYFNSMIQYTWRRD 839

RESULT 12

US-10-190-417-9
 ; Sequence 9, Application US/10190417
 ; Publication No. US20030166137A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zuker, Charles S.
 ; APPLICANT: Ryba, Nicholas J. P.
 ; APPLICANT: Chandrashekar, Jayaram
 ; APPLICANT: Hoon, Mark A.
 ; APPLICANT: Nelson, Greg
 ; APPLICANT: Zhang, Yifeng
 ; APPLICANT: The Regents of the University of California
 ; APPLICANT: The Government of the United States of America
 ; APPLICANT: as represented by the Secretary of the
 ; APPLICANT: Department of Health and Human Services
 ; TITLE OF INVENTION: Mammalian Sweet and Amino Acid Heterodimeric Taste
 ; TITLE OF INVENTION: Receptors
 ; FILE REFERENCE: 02307E-120130US
 ; CURRENT APPLICATION NUMBER: US/10/190,417
 ; CURRENT FILING DATE: 2002-11-14
 ; PRIOR APPLICATION NUMBER: US 60/302,898
 ; PRIOR FILING DATE: 2001-07-03
 ; PRIOR APPLICATION NUMBER: US 09/927,315
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: US 60/358,925
 ; PRIOR FILING DATE: 2002-02-22

; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 9
 ; LENGTH: 838
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human T1R2
 US-10-190-417-9

Query Match 98.9%; Score 4392.5; DB 14; Length 838;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 833; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
 QY 1 MGPRAKTICSLFLLWLAEPANESDFVLPDYLGLGGLFSLHANMKGVHNLFLQVPWCK 60
 DB 1 MGPRAKTICSLFLLWLAEPANESDFVLPDYLGLGGLFSLHANMKGVHNLFLQVPWCK 60
 QY 61 EYEVKIVGNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN 120
 DB 61 EYEVKIVGNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN 120
 QY 121 LPIQEDYSNYSRVVAVIGPNSVMTVANFLSLFLLPQITYSAISDELADKVRFPAL 180
 DB 121 LPIQEDYSNYSRVVAVIGPNSVMTVANFLSLFLLPQITYSAISDELADKVRFPAL 180
 QY 181 LRTTPEADHVEAMVQLMHLFRNWIIVLVSSDTYGRNGQLLGERVARRDICIATFQETL 240
 DB 181 LRTTPEADHVEAMVQLMHLFRNWIIVLVSSDTYGRNGQLLGERVARRDICIATFQETL 240
 QY 241 PTLQPNQNTSEERQRLVTIVDKLQOSTARVVVVFSPDLTYHFFNEVLQNFTGAVWIA 300
 DB 241 PTLQPNQNTSEERQRLVTIVDKLQOSTARVVVVFSPDLTYHFFNEVLQNFTGAVWIA 300
 QY 301 SESWALDVLNHLTEGLHGLTGLTIGTOSVPIPGSESEREWCPQAGPPPLRTSOSYTCN 360
 DB 301 SESWALDVLNHLTEGLHGLTGLTIGTOSVPIPGSESEREWCPQAGPPPLRTSOSYTCN 360
 QY 361 QECNCLNATLSFNTILRLSGERVVYSVAVYVAHAHALSHLGLGDKTCTKRVVYPWQL 420
 DB 361 QECNCLNATLSFNTILRLSGERVVYSVAVYVAHAHALSHLGLGDKTCTKRVVYPWQL 420
 QY 421 LEEIKVNFNTLLDQIFPDQGDVALHLEIVQWQWDRSQNPFQSVASYPLQRLKNIQD 480
 DB 421 LEEIKVNFNTLLDQIFPDQGDVALHLEIVQWQWDRSQNPFQSVASYPLQRLKNIQD 480
 QY 481 ISWHTVNNTPIMSMCKSKCQSGQKKKPGVGHVCCFECIDCLPGTFLNTEDEYECQACP 540
 DB 481 ISWHTVNNTPIMSMCKSKCQSGQKKKPGVGHVCCFECIDCLPGTFLNTEDEYECQACP 540
 QY 541 NEWSYQSETSCFKQLVFLWEHAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
 DB 541 NEWSYQSETSCFKQLVFLWEHAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
 QY 601 GPMCFMLTLLLVAMVVPVVPKPVSTCLCRQALFPLCTICISCIATVRSFQIVCAFK 660
 DB 601 GPMCFMLTLLLVAMVVPVVPKPVSTCLCRQALFPLCTICISCIATVRSFQIVCAFK 660
 QY 661 MASFPFRAYSVMVRYQGPVYSMAFTVLKMWIVVIGMLATGLSPTRTDPPDKITIVSC 720
 DB 661 MASFPFRAYSVMVRYQGPVYSMAFTVLKMWIVVIGMLARQPS-HPRTDPPDKITIVSC 719
 QY 721 NPYNRSLLFNTSLDLLLSVVGFSFAYMGKELPTNYNEAKITILSMTFYFTSSVSLCTFM 780
 DB 720 NPYNRSLLFNTSLDLLLSVVGFSFAYMGKELPTNYNEAKITILSMTFYFTSSVSLCTFM 779
 QY 781 SAYSGVLVTIVDLVTLNLAISLGVFGPKCYMILFYPERNTPAYFNMSIQGYTMRD 839
 DB 780 SAYSGVLVTIVDLVTLNLAISLGVFGPKCYMILFYPERNTPAYFNMSIQGYTMRD 838

RESULT 13
 US-10-124-598-7

; Sequence 7, Application US/10124598
 ; Publication No. US20020119526A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zuker, Charles S.
 ; APPLICANT: Adler, Jon Elliot
 ; APPLICANT: Lindemeier, Juergen
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
 ; TITLE OF INVENTION: Involved in Sensory Transduction
 ; FILE REFERENCE: 02307E-088720US
 ; CURRENT APPLICATION NUMBER: US/10/124,598
 ; CURRENT FILING DATE: 2002-04-16
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/361,631
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-27
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/112,747
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-17
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 669
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human G-protein coupled receptor (GPCR) B4 amino
 ; OTHER INFORMATION: acid sequence
 US-10-124-598-7

Query Match 78.0%; Score 3463.5; DB 13; Length 669;
 Best Local Similarity 97.5%; Pred. No. 4.5e-301;
 Matches 661; Conservative 1; Mismatches 7; Indels 9; Gaps 3;
 QY 162 ITYSAISDELKDKVFPALLRTTTPSADHVEAMVQLMHLFRNWIIVLVSSDTYGRNGQ 221
 DB 1 ITYSAISDELKDKVFPALLRTTTPSADHVEAMVQLMHLFRNWIIVLVSSDTYGRNGQ 60
 QY 222 LLGERVARRDICIATFQETLPTLQPNQNTSEERQRLVTIVDKLQOSTARVVVVFSPDLT 281
 DB 61 LLGERVARRDICIATFQETLPTLQPNQNTSEERQRLVTIVDKLQOSTARVVVVFSPDLT 120
 QY 282 YHFFNEVLQNFTGAVMIASESWAIDPVLNHLTEGLHGLTGLTIGTOSVPIPGSESEREW 341
 DB 121 YHFFNEVLQNFTGAVMIASESWAIDPVLNHLTEGLHGLTGLTIGTOSVPIPGSESEREW 180
 QY 342 GPOAGPPLSSTOSYTCNQCNDCLNATLSFNTILRLSGERVVYSVAVYVAHAHALS 401
 DB 181 GPOAGPPLSSTOSYTCNQCNDCLNATLSFNTILRLSGERVVYSVAVYVAHAHALS 240
 QY 402 LLGCDKSTCTKRVVYPWQLLEEIKVNFNTLLDQIFPDQGDVALHLEIVQWQWDRSQN 461
 DB 241 LLGCDKSTCTKRVVYPWQLLEEIKVNFNTLLDQIFPDQGDVALHLEIVQWQWDRSQN 300
 QY 462 FQSVASYPLQRLKNIQD ISWHTVNNTPIMSMCKSKCQSGQKKKPGVGHVCCFECIDCL 521
 DB 301 FQSVASYPLQRLKNIQD-TSLHTVNNTPIMSMCKSKCQSGQKKKPGVGHVCCFECIDCL 359
 QY 522 PGTFLNHTEDEYECQACPNEWSYQSETSCFKQLVFLWEHAPTIAVALLAALGFLSTL 581
 DB 360 PGTFLNHTEDEYECQACPNEWSYQSETSCFKQLVFLWEHAPTIAVALLAALGFLSTL 412
 QY 582 AILVIFWRHFQTPIVRSAGGPMCFMLTLLLVAMVVPVVPKPVSTCLCRQALFPLCF 641
 DB 413 AILVIFWRHFQTPIVRSAGGPMCFMLTLLLVAMVVPVVPKPVSTCLCRQALFPLCF 472
 QY 642 TICISCIATVRSFQIVCAFKMASFPFRAYSVMVRYQGPVYSMAFTVLKMWIVVIGMLATG 701
 DB 473 TICISCIATVRSFQIVCAFKMASFPFRAYSVMVRYQGPVYSMAFTVLKMWIVVIGMLAR 532
 QY 702 LSPTRTDPPDKITIVSCNPYNRSLLFNTSLDLLLSVVGFSFAYMGKELPTNYNEAKP 761
 DB 533 QS-HPRTDPPDKITIVSCNPYNRSLLFNTSLDLLLSVVGFSFAYMGKELPTNYNEAKP 591
 QY 762 ITLSMTFYFTSSVSLCTFMSAYSGVLVTIVDLVTLNLAISLGVFGPKCYMILFYPER 821

Db 592 ITLSMTFYFTSSVSLCTFMSAYSGLVLTIVDILLVTLNLLAISLGYPGPKCYMILFYPER 651
QY 822 NTPAYFNSMIQGYTMRD 839
Db 652 NTPAYFNSMIQGYTMRD 669

RESULT 14

US-10-096-144-7
; Sequence 7, Application US/10096144
; Publication No. US20030022288A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Lindemeier, Juergen
; APPLICANT: Adler, Jon Elliot
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; TITLE OF INVENTION: Involved in Sensory Transduction
; FILE REFERENCE: 02307E-088720US
; CURRENT APPLICATION NUMBER: US/10/096,144
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/361,631
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/095,464
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/112,747
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 7
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) B4 amino
; OTHER INFORMATION: acid sequence
US-10-096-144-7

Query Match 78.0%; Score 3463.5; DB 14; Length 669;
Best Local Similarity 97.5%; Pred. No. 4.5e-301;
Matches 661; Conservative 1; Mismatches 7; Indels 9; Gaps 3;
QY 162 ITYSAISDELDRKVRFPALLRTTSPADHVEAMVQLMHLFRWNWIIIVLVSSDTYGRDNGQ 221
Db 1 ITYSAISDELDRKVRFPALLRTTSPADHVEAMVQLMHLFRWNWIIIVLVSSDTYGRDNGQ 60
QY 222 LLGERVARRDICIATFQETLPTLPQNQNTSEERQRLTVIVDKLQOSTARVVVVFSPDLTL 281
Db 61 LLGERVARRDICIATFQETLPTLPQNQNTSEERQRLTVIVDKLQOSTARVVVVFSPDLTL 120
QY 282 YHFFNEVLNQFTGAVWIASWAIIDVHLNLTGLHGTFLGTTIOSVPIPGSEPREW 341
Db 121 YHFFNEVLNQFTGAVWIASWAIIDVHLNLTGLHGTFLGTTIOSVPIPGSEPREW 180
QY 342 GPQAGPPPLSRTSOSYTCNQCNDCLNATLSFNTILRSGERVVYVSAYVAHALHS 401
Db 181 GPQAGPPPLSRTSOSYTCNQCNDCLNATLSFNTILRSGERVVYVSAYVAHALHS 240
QY 402 LLGCDKSTCKRVVYPMQLLEEIKWVNTLIDHGFDPQGDVALHLEIVQWQDRSQNP 461
Db 241 LLGCDKSTCKRVVYPMQLLEEIKWVNTLIDHGFDPQGDVALHLEIVQWQDRSQNP 300
QY 462 FQSVASYPLQRLQKNTQDISWHTVNTTIPMSMCKSCQSGKKKPVGIHVCCFECIDCL 521
Db 301 FQSVASYPLQRLQKNTQDISWHTVNTTIPMSMCKSCQSGKKKPVGIHVCCFECIDCL 359
QY 522 PGTFLNHTEDYEYEQACPNNEWSQSETSCFKRLVFLWEHEAPTIAVALLAALGFLSTL 581
Db 360 PGTFLNHTEDYEYEQACPNNEWSQSETSCFKRLVFLWEHEAPTIAVALLAALGFLSTL 412
QY 582 AILVIFWRHFTPIVRSGGPMCFMLTLVAVVAVVYVGGPKVSTCLCRQALFPLCF 641
Db 413 AILVIFWRHFTPIVRSGGPMCFMLTLVAVVAVVYVGGPKVSTCLCRQALFPLCF 472

QY 642 TICISCIAYRSFOIVCAFKMASRFPFRAYSVWRYQGYVSMAFITVLKMWIVVIGMLATG 701
Db 473 TICISCIAYRSFOIVCAFKMASRFPFRAYSVWRYQGYVSMAFITVLKMWIVVIGMLARP 532
QY 702 LSPTTETDDPKITIVSCNPNYRNLSLNTSLLDLSLVVGFSAFMGKELPTNYNEAKF 761
Db 533 QS-HPRTPDDPKITIVSCNPNYRNLSLNTSLLDLSLVVGFSAFMGKELPTNYNEAKF 591
QY 762 ITLSMTFYFTSSVSLCTFMSAYSGLVLTIVDILLVTLNLLAISLGYPGPKCYMILFYPER 821
Db 592 ITLSMTFYFTSSVSLCTFMSAYSGLVLTIVDILLVTLNLLAISLGYPGPKCYMILFYPER 651
QY 822 NTPAYFNSMIQGYTMRD 839
Db 652 NTPAYFNSMIQGYTMRD 669

RESULT 15

US-10-225-567A-683
; Sequence 683, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 683
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-683

Query Match 78.0%; Score 3463.5; DB 14; Length 669;
Best Local Similarity 97.5%; Pred. No. 4.5e-301;
Matches 661; Conservative 1; Mismatches 7; Indels 9; Gaps 3;
QY 162 ITYSAISDELDRKVRFPALLRTTSPADHVEAMVQLMHLFRWNWIIIVLVSSDTYGRDNGQ 221
Db 1 ITYSAISDELDRKVRFPALLRTTSPADHVEAMVQLMHLFRWNWIIIVLVSSDTYGRDNGQ 60
QY 222 LLGERVARRDICIATFQETLPTLPQNQNTSEERQRLTVIVDKLQOSTARVVVVFSPDLTL 281
Db 61 LLGERVARRDICIATFQETLPTLPQNQNTSEERQRLTVIVDKLQOSTARVVVVFSPDLTL 120
QY 282 YHFFNEVLNQFTGAVWIASWAIIDVHLNLTGLHGTFLGTTIOSVPIPGSEPREW 341
Db 121 YHFFNEVLNQFTGAVWIASWAIIDVHLNLTGLHGTFLGTTIOSVPIPGSEPREW 180
QY 342 GPQAGPPPLSRTSOSYTCNQCNDCLNATLSFNTILRSGERVVYVSAYVAHALHS 401
Db 181 GPQAGPPPLSRTSOSYTCNQCNDCLNATLSFNTILRSGERVVYVSAYVAHALHS 240
QY 402 LLGCDKSTCKRVVYPMQLLEEIKWVNTLIDHGFDPQGDVALHLEIVQWQDRSQNP 461
Db 241 LLGCDKSTCKRVVYPMQLLEEIKWVNTLIDHGFDPQGDVALHLEIVQWQDRSQNP 300
QY 462 FQSVASYPLQRLQKNTQDISWHTVNTTIPMSMCKSCQSGKKKPVGIHVCCFECIDCL 521
Db 301 FQSVASYPLQRLQKNTQDISWHTVNTTIPMSMCKSCQSGKKKPVGIHVCCFECIDCL 359
QY 522 PGTFLNHTEDYEYEQACPNNEWSQSETSCFKRLVFLWEHEAPTIAVALLAALGFLSTL 581
Db 360 PGTFLNHTEDYEYEQACPNNEWSQSETSCFKRLVFLWEHEAPTIAVALLAALGFLSTL 412

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